

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:59 ; Search time 10 Seconds
(without alignments)
105.923 Million cell updates/sec

Title: US-09-445-576A-38

Perfect score: 183

Sequence: 1 RRVKEDGDLKTQVEKLRVNAKEMQALQTVCLR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	166	90.7	197	4	US-09-602-877A-99
2	79	43.2	202	1	US-08-469-486-56
3	79	43.2	202	2	US-08-469-658-56
4	62	33.9	84	1	US-08-452-592B-8
5	59	32.2	84	1	US-08-452-592B-9
6	58	31.7	84	1	US-08-452-592B-7
7	54	29.5	84	1	US-08-452-592B-10
8	52	28.4	76	3	US-08-956-307B-18
9	52	28.4	367	4	US-08-845-258-20
10	52	28.4	367	4	US-08-845-258-49
11	52	28.4	367	4	US-08-990-571-20
12	52	28.4	367	4	US-08-990-571-49
13	52	28.4	367	4	US-08-723-142A-20
14	52	28.4	367	4	US-08-723-142A-49
15	52	28.4	367	4	US-09-528-784A-20
16	52	28.4	367	4	US-09-528-784A-49
17	51.5	28.1	1312	2	US-08-592-126-148
18	51.5	28.1	1312	2	US-08-687-080-51
19	51	27.9	42	3	US-08-956-307B-2
20	50.5	27.6	2161	1	US-07-745-206A-2
21	50.5	27.6	2161	1	US-08-455-543A-49
22	50.5	27.6	2161	1	US-08-455-543A-51
23	50.5	27.6	2161	2	US-08-223-305C-49
24	50.5	27.6	2161	2	US-08-223-305C-51
25	50.5	27.6	2161	2	US-08-311-363-2
26	50	27.3	84	1	US-08-452-592B-6
27	50	27.3	424	2	US-08-951-148-9

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28 50 27.3 424 2 US-09-165-234-9 Sequence 9, Appli
29 50 27.3 424 3 US-09-274-570-9 Sequence 9, Appli
30 50 27.3 529 1 US-08-178-477B-32 Sequence 32, Appli
31 50 27.3 529 4 US-09-304-121-2 Sequence 2, Appli
32 50 27.3 783 4 US-09-513-783A-176 Sequence 176, App
33 49 26.8 77 1 US-08-178-477B-29 Sequence 29, Appli
34 49 26.8 466 4 US-09-610-401-4 Sequence 4, Appli
35 49 26.8 691 1 US-08-178-477B-2 Sequence 2, Appli
36 48.5 26.5 422 4 US-09-071-035-484 Sequence 484, App
37 48.5 26.5 449 4 US-09-071-035-482 Sequence 482, App
38 48 26.2 76 3 US-08-956-307B-17 Sequence 17, Appli
39 48 26.2 1010 4 US-09-134-001C-5178 Sequence 5178, Ap
40 48 26.2 1786 4 US-08-973-462-8 Sequence 8, Appli
41 47 25.7 42 3 US-08-956-307B-1 Sequence 1, Appli
42 47 25.7 411 2 US-08-713-815A-4 Sequence 4, Appli
43 47 25.7 441 2 US-08-713-815A-3 Sequence 3, Appli
44 47 25.7 466 4 US-09-610-401-3 Sequence 3, Appli
45 47 25.7 851 1 US-08-369-796-2 Sequence 2, Appli

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ALIGNMENTS

RESULT 1

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US-09-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; TYPE: PRT
; ORGANISM: Homo sapien
; LENGTH: 197
US-09-602-877A-99

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Query Match          90.7%   Score 166;   DB 4;   Length 197;
Best Local Similarity 86.1%   Pred. No. 5.9e-15;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 RRVKEDGDLKTQVEKLRVNAKEMQALQTVCLR 36
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Db 35 RRVKEDGDLKTQVEKLRVNAKEMQALQTVCLR 70

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RESULT 2

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US-08-469-486-56
; Sequence 56, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoeversen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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QY 3 VKEKDGDKTOVEKLRVNAKEMQA 29
:| | | | | :| | | | | :| | | | | :| | | | |
Db 39 LKAKIGDLKNKVAQLEREVRSKDKAA 65

RESULT 5

US-08-452-592B-9
; Sequence 9, Application US/08452592B
; Patent No. 5712366
; GENERAL INFORMATION:
; APPLICANT: McGrath, Kevin P.
; APPLICANT: Kaplan, David L.
; TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
; TITLE OF INVENTION: Self-Assembling Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Soldier Systems Command
; STREET: AMSCC-CC (Patent Counsel)
; CITY: Natick
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01760-5035
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: WordPerfect Version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,592B
; FILING DATE: 25 May 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,948
; FILING DATE: 25 May 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, Richard J.
; NAME: Lamming, John H.
; NAME: Ranucci, Vincent J.
; REGISTRATION NUMBER: 22,062 (Donahue)
; REGISTRATION NUMBER: 34,857 (Lamming)
; REGISTRATION NUMBER: 29,579 (Ranucci)
; REFERENCE/DOCKET NUMBER: NA-1096D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-233-4510
; TELEFAX: 508-233-5167
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-452-592B-9

Query Match 32.28; Score 59; DB 1; Length 84;
Best Local Similarity 48.19; Pred. No. 0.47;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 VKEKDGDKTOVEKLRVNAKEMQA 29
:| | | | | :| | | | | :| | | | | :| | | | |
Db 39 LKAKIGDLENEVAQLEREVRSKDKAA 65

RESULT 6

US-08-452-592B-7
; Sequence 7, Application US/08452592B
; Patent No. 5712366
; GENERAL INFORMATION:
; APPLICANT: McGrath, Kevin P.
; APPLICANT: Kaplan, David L.
; TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
; TITLE OF INVENTION: Self-Assembling Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Soldier Systems Command

; STREET: AMSCC-CC (Patent Counsel)
; CITY: Natick
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01760-5035
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: WordPerfect Version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,592B
; FILING DATE: 25 May 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,948
; FILING DATE: 25 May 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, Richard J.
; NAME: Lamming, John H.
; NAME: Ranucci, Vincent J.
; REGISTRATION NUMBER: 22,062 (Donahue)
; REGISTRATION NUMBER: 34,857 (Lamming)
; REGISTRATION NUMBER: 29,579 (Ranucci)
; REFERENCE/DOCKET NUMBER: NA-1096D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-233-4510
; TELEFAX: 508-233-5167
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-452-592B-7

Query Match 31.78; Score 58; DB 1; Length 84;
Best Local Similarity 48.19; Pred. No. 0.64;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 VKEKDGDKTOVEKLRVNAKEMQA 29
:| | | | | :| | | | | :| | | | | :| | | | |
Db 39 LKAKIGDLKNKVAQLKRKRVRSLKDKAA 65

RESULT 7

US-08-452-592B-10
; Sequence 10, Application US/08452592B
; Patent No. 5712366
; GENERAL INFORMATION:
; APPLICANT: McGrath, Kevin P.
; APPLICANT: Kaplan, David L.
; TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
; TITLE OF INVENTION: Self-Assembling Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Soldier Systems Command
; STREET: AMSCC-CC (Patent Counsel)
; CITY: Natick
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01760-5035
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: DOS 6.22
; SOFTWARE: WordPerfect Version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,592B
; FILING DATE: 25 May 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,948
; FILING DATE: 25 May 1993

ATTORNEY/AGENT INFORMATION:
 NAME: Donahue, Richard J.
 NAME: Lamming, John H.
 NAME: Ranucci, Vincent J.
 REGISTRATION NUMBER: 22,062 (Donahue)
 REGISTRATION NUMBER: 34,857 (Lamming)
 REGISTRATION NUMBER: 29,579 (Ranucci)
 REFERENCE/DOCKET NUMBER: NA-1096D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 508-233-4510
 TELEFAX: 508-233-5167
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-452-592B-10

Query Match 29.5%; Score 54; DB 1; Length 84;
 Best Local Similarity 44.4%; Pred. No. 2.2;
 Matches 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 3 VKEKGDGLKTQVEKLRVNAKEMQA 29
 DB 39 LKAKIGDLENEVAQLREVRSLDEZAA 65

RESULT 8
 US-08-956-307B-18
 Sequence 18, Application US/08956307B
 Patent No. 6090911
 GENERAL INFORMATION:
 APPLICANT: Petka, Wendy A.
 APPLICANT: Tirrell, David A.
 APPLICANT: Kevin P. McGrath
 TITLE OF INVENTION: REVERSIBLE HYDROGELS
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,307B
 FILING DATE: 22-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fasse, J. Peter
 REGISTRATION NUMBER: 32,983
 REFERENCE/DOCKET NUMBER: 07880/033001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 76 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-956-307B-18

Query Match 28.4%; Score 52; DB 3; Length 76;
 Best Local Similarity 46.2%; Pred. No. 3.6;

Matches 12; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 KKKDGLKTQVEKLRVNAKEMQA 29
 DB 17 KWASGDLKNKVAQLKKVRSLDKAA 42

RESULT 9
 US-08-845-258-20
 Sequence 20, Application US/08845258
 Patent No. 6183976
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Houghton, Raymond
 APPLICANT: Sleath, Paul R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED AND BERRY
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/845,258
 FILING DATE: 24-APR-1997
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.426C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 367 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-845-258-20

Query Match 28.4%; Score 52; DB 4; Length 367;
 Best Local Similarity 36.0%; Pred. No. 22;
 Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 RVKEKGDGLKTQVEKLRVNAKKE 26
 DB 280 KITRKDGDYNTHFEDMIKELNSAAE 304

RESULT 10
 US-08-845-258-49
 Sequence 49, Application US/08845258
 Patent No. 6183976
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Houghton, Raymond
 APPLICANT: Sleath, Paul R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED AND BERRY


```

; TYPE: amino acid

```

; NUMBER OF SEQUENCES: 49

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SEED AND BERRY
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/723,142A
;; APPLICATION NUMBER: US/08/723,142A
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Makl, David J.
;; REGISTRATION NUMBER: 31,392
;; REFERENCE/DOCKET NUMBER: 210121.426
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 367 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-08-723-142A-20

Query Match 28.4%; Score 52; DB 4; Length 367;
Best Local Similarity 36.0%; Pred. No. 22;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 2 RVKEKDGDLKTQVEKLMREVNALKE 26
Db 280 KITKKGDNTHFEDMIKELNSAAE 304

RESULT 14
US-08-723-142A-49
;; Sequence 49, Application US/08/723142A
;; Patent No. 6306396
;; GENERAL INFORMATION:
;; APPLICANT: Reed, Steven G.
;; APPLICANT: Lodes, Michael J.
;; APPLICANT: Houghton, Raymond
;; APPLICANT: Sleath, Paul R.
;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
;; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
;; NUMBER OF SEQUENCES: 49
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SEED AND BERRY
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/723,142A
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Makl, David J.
;; REGISTRATION NUMBER: 31,392
;; REFERENCE/DOCKET NUMBER: 210121.426
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 49:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 367 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-723-142A-49

Query Match 28.4%; Score 52; DB 4; Length 367;
Best Local Similarity 36.0%; Pred. No. 22;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 2 RVKEKDGDLKTQVEKLMREVNALKE 26
Db 280 KITKKGDNTHFEDMIKELNSAAE 304

RESULT 15
US-09-528-784A-20
;; Sequence 20, Application US/09528784A
;; Patent No. 6451315
;; GENERAL INFORMATION:
;; APPLICANT: Reed, Steven G.
;; APPLICANT: Lodes, Michael J.
;; APPLICANT: Houghton, Raymond L.
;; APPLICANT: Sleath, Paul R.
;; APPLICANT: McNeill, Patricia D.
;; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
;; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
;; FILE REFERENCE: 210121.426C4
;; CURRENT APPLICATION NUMBER: US/09/528,784A
;; CURRENT FILING DATE: 2000-03-17
;; NUMBER OF SEQ ID NOS: 90
;; SOFTWARE: PastSEQ for Windows Version 3.0
;; SEQ ID NO 20
;; LENGTH: 367
;; TYPE: PRT
;; ORGANISM: Babesia microti
US-09-528-784A-20

Query Match 28.4%; Score 52; DB 4; Length 367;
Best Local Similarity 36.0%; Pred. No. 22;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 2 RVKEKDGDLKTQVEKLMREVNALKE 26
Db 280 KITKKGDNTHFEDMIKELNSAAE 304

Search completed: April 15, 2003, 11:51:50
Job time : 11 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:50:25 ; Search time 10 Seconds
(without alignments)
220.090 Million cell updates/sec

Title: US-09-445-576A-38
Perfect score: 183
Sequence: 1 RRVKEDGDLKTQVEKLWREVNALKEMQALQTVCLR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PublishedApplications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	183	100.0	36	US-09-987-107-41	Sequence 41, Appl
2	166	90.7	197	10 US-09-745-288-99	Sequence 99, Appl
3	166	90.7	206	9 US-09-938-418-10	Sequence 10, Appl
4	166	90.7	206	9 US-09-992-598-403	Sequence 403, Appl
5	166	90.7	206	9 US-09-989-293A-403	Sequence 403, Appl
6	166	90.7	206	9 US-09-989-735-403	Sequence 403, Appl
7	166	90.7	206	9 US-09-990-444-403	Sequence 403, Appl
8	166	90.7	206	9 US-09-989-730-403	Sequence 403, Appl
9	166	90.7	206	9 US-09-990-436-403	Sequence 403, Appl
10	166	90.7	206	9 US-09-991-181-403	Sequence 403, Appl
11	166	90.7	206	9 US-09-993-687-403	Sequence 403, Appl
12	166	90.7	206	9 US-09-989-734-403	Sequence 403, Appl
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14	166	90.7	206	9 US-09-997-653-403	Sequence 403, Appl
15	166	90.7	206	9 US-10-174-590-276	Sequence 276, Appl
16	166	90.7	206	9 US-10-176-758-276	Sequence 276, Appl
17	166	90.7	206	9 US-10-175-737-276	Sequence 276, Appl
18	166	90.7	206	9 US-09-993-667-403	Sequence 403, Appl
19	166	90.7	206	9 US-10-173-706-276	Sequence 276, Appl

20	166	90.7	206	9	US-10-175-738-276	Sequence 276, App
21	166	90.7	206	9	US-10-175-752-276	Sequence 276, App
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24	166	90.7	206	9	US-10-176-913-276	Sequence 276, App
25	166	90.7	206	9	US-10-180-552-276	Sequence 276, App
26	166	90.7	206	9	US-10-180-557-276	Sequence 276, App
27	166	90.7	206	9	US-09-990-438-403	Sequence 403, App
28	166	90.7	206	9	US-09-990-562-403	Sequence 403, App
29	166	90.7	206	9	US-09-997-428-403	Sequence 403, App
30	166	90.7	206	9	US-09-997-666-403	Sequence 276, App
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36	166	90.7	206	9	US-10-175-739-276	Sequence 276, App
37	166	90.7	206	9	US-10-175-740-276	Sequence 276, App
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42	166	90.7	206	9	US-10-176-750-276	Sequence 276, App
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ALIGNMENTS

RESULT 1
US-09-987-107-41
; Sequence 41, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
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; ORGANISM: Bos taurus
US-09-987-107-41
Query Match 100.0% Score 183; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.le-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 RRVKEDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
RESULT 2
US-09-745-288-99
; Sequence 99, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Stevan G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

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; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-745-288-99

Query Match          90.7%; Score 166; DB 10; Length 197;
Best Local Similarity 86.1%; Pred. No. 3.4e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 35 RRVKKGDLKQVEKLVREVNALKEMOALQTVCLR 70

RESULT 3
US-09-938-418-10
; Sequence 10, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Polakis, Paul
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
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; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
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; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-418-10

Query Match          90.7%; Score 166; DB 9; Length 206;
Best Local Similarity 86.1%; Pred. No. 3.6e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKKGDLKQVEKLVREVNALKEMOALQTVCLR 36
Db 44 RRVKKGDLKQVEKLVREVNALKEMOALQTVCLR 79

RESULT 4
US-09-992-598-403
; Sequence 403, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730F1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 90.7%; Score 166; DB 9; Length 206;
Best Local Similarity 86.1%; Pred. No. 3.6e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5

US-09-989-293A-403
; Sequence 403, Application US/0989293A

; Patent No. US2002017164A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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3	PRIOR APPLICATION NUMBER: 60/091978	
3	PRIOR FILING DATE: 1998-07-07	
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3	PRIOR FILING DATE: 1998-07-07	

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; PRIOR APPLICATION NUMBER: 50/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      93.7%; Score 166; DB
Best Local Similarity 85.1%; Pred. No. 3.6e-
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DB 44 RRVDRXGDKLTKQIEKLRTEVNALKEIQALQTVCLR 79

RESULT 6
US-989-735-403
; Sequence 403, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P161
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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23	PRIOR FILING DATE: 1998-06-10	
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40	PRIOR APPLICATION NUMBER: 60/089105	
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?	PRIOR FILING DATE: 1998-07-07
?	PRIOR APPLICATION NUMBER: 60/091982
?	PRIOR FILING DATE: 1998-07-07
?	PRIOR APPLICATION NUMBER: 60/092182
?	PRIOR FILING DATE: 1998-07-09

Query Match	90.7%	Score 166;	DB 9;	Length 206;
Best Local Similarity	86.1%	Pred. No. 3.6e-14;		
Matches 31; Conservative		Mismatches 4;	Indels 1;	

QY 1 RRVKKGDLKTQVEKLRNVALKEMOALQTVCLR 36
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DB 44 RVRDGDGLKTQIEKLRNVALKEMOALQTVCLR 79

RESULT 7

US-09-990-444-403

; Sequence 403, Application US/09990444

; Publication No. US20020193300A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C19

; CURRENT APPLICATION NUMBER: US/09/990,444

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087759

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/087827

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/088021

; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088026

; PRIOR FILING DATE: 1998-06-04

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;; PRIOR FILING DATE: 1998-06-22
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 90.7%; Score 166; DB 9; Length 206;
Best Local Similarity 86.1%; Pred. No. 3.6e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RRVKEGDGLKTQVEKLVREVNALKEQALQTVCLR 36
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Db 44 RRVKDGDLKTQIEKLVREVNALKEQALQTVCLR 79
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RESULT 8
US-09-989-730-403

;; Sequence 403, Application US/09989730
;; Publication No. US20020197674A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C69
;; CURRENT APPLICATION NUMBER: US/09/989,730
;; PRIOR FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 90.7%; Score 166; DB 9; Length 206;
Best Local Similarity 86.1%; Pred. No. 3.6e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKEDGDLKTQVEKLRWREYNALKEMOALQTVCLR 36
Db 44 RRVKEDGDLKTQVEKLRWREYNALKEMOALQTVCLR 79

RESULT 9

US-09-990-436-403
; Sequence 403, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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Query Match 90.7%; Score 166; DB 9; Length 206;
Best Local Similarity 86.1%; Pred. NO. 3.6e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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RESULT 11
US-09-993-687-403
; Sequence 403, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
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Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14

US-09-997-653-403
Sequence 403, Application US/0997653
Publication No. US2003008297A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC38

CURRENT APPLICATION NUMBER: US/09/997,653

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:05 ; Search time 183 Seconds
(without alignments)
126.833 Million cell updates/sec

Title: US-09-445-576A-38

Perfect score: 183

Sequence: 1 RRVKRDGDLTKQVEXKLRVFNALKEMQALQTVCLR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
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- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	183	100.0	36	18 US-09-445-576-37	Sequence 37, Appl
2	183	100.0	36	23 US-09-987-107-41	Sequence 41, Appl
3	183	100.0	197	21 US-09-791-537-145359	Sequence 145359,
4	166	90.7	197	1 PCT-US02-19669-55	Sequence 55, Appl
5	166	90.7	197	16 US-09-288-950-99	Sequence 99, Appl
6	166	90.7	197	17 US-09-346-327-99	Sequence 99, Appl

7	166	90.7	137	20	US-09-687-507-99	Sequence 99, Appl
8	166	90.7	137	20	US-09-687-507A-99	Sequence 99, Appl
9	166	90.7	137	21	US-09-745-288-99	Sequence 99, Appl
10	166	90.7	137	21	US-09-778-381-99	Sequence 99, Appl
11	166	90.7	137	21	US-09-791-537-25686	Sequence 25686, A
12	166	90.7	137	25	US-10-177-293-55	Sequence 55, Appl
13	166	90.7	206	1	PCT-US02-12619-2	Sequence 2, Appl
14	166	90.7	206	1	PCT-US02-19669-57	Sequence 57, Appl
15	166	90.7	206	21	US-09-709-238-403	Sequence 403, Appl
16	166	90.7	206	23	US-09-938-418-10	Sequence 10, Appl
17	166	90.7	206	23	US-09-941-992-403	Sequence 403, Appl
18	166	90.7	206	23	US-09-989-279-403	Sequence 403, Appl
19	166	90.7	206	23	US-09-989-293A-403	Sequence 403, Appl
20	166	90.7	206	23	US-09-989-328-403	Sequence 403, Appl
21	166	90.7	206	23	US-09-989-721-403	Sequence 403, Appl
22	166	90.7	206	23	US-09-989-722-403	Sequence 403, Appl
23	166	90.7	206	23	US-09-989-723-403	Sequence 403, Appl
24	166	90.7	206	23	US-09-989-724-403	Sequence 403, Appl
25	166	90.7	206	23	US-09-989-725-403	Sequence 403, Appl
26	166	90.7	206	23	US-09-989-726-403	Sequence 403, Appl
27	166	90.7	206	23	US-09-989-727-403	Sequence 403, Appl
28	166	90.7	206	23	US-09-989-728-403	Sequence 403, Appl
29	166	90.7	206	23	US-09-989-729A-403	Sequence 403, Appl
30	166	90.7	206	23	US-09-989-730-403	Sequence 403, Appl
31	166	90.7	206	23	US-09-989-731-403	Sequence 403, Appl
32	166	90.7	206	23	US-09-989-732-403	Sequence 403, Appl
33	166	90.7	206	23	US-09-989-734-403	Sequence 403, Appl
34	166	90.7	206	23	US-09-989-735-403	Sequence 403, Appl
35	166	90.7	206	23	US-09-989-862-403	Sequence 403, Appl
36	166	90.7	206	23	US-09-990-427-403	Sequence 403, Appl
37	166	90.7	206	23	US-09-990-436-403	Sequence 403, Appl
38	166	90.7	206	23	US-09-990-437-403	Sequence 403, Appl
39	166	90.7	206	23	US-09-990-438-403	Sequence 403, Appl
40	166	90.7	206	23	US-09-990-439-403	Sequence 403, Appl
41	166	90.7	206	23	US-09-990-440-403	Sequence 403, Appl
42	166	90.7	206	23	US-09-990-441-403	Sequence 403, Appl
43	166	90.7	206	23	US-09-990-442-403	Sequence 403, Appl
44	166	90.7	206	23	US-09-990-443-403	Sequence 403, Appl
45	166	90.7	206	23	US-09-990-444-403	Sequence 403, Appl

ALIGNMENTS

RESULT 1
US-09-445-576-37
; Sequence 37, Application. US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Heilskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjoller
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN =1
; CURRENT APPLICATION NUMBER: US/09/445,576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 36
; TYPE: PRT
; ORGANISM: bovine
US-09-445-576-37

Query Match 100.0%; Score 183; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36

RESULT 2

US-09-987-107-41
; Sequence 41, Application US/09987107
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: 2001-11-13
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-987-107-41

Query Match 100.0%; Score 183; DB 23; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36

RESULT 3

US-09-791-537-145359
; Sequence 145359, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bloncomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 145359
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-791-537-145359

Query Match 100.0%; Score 183; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 35 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 70

RESULT 4

PCT-US02-19669-55
; Sequence 55, Application PC/TUS0219669
; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669-55

Query Match 90.7%; Score 166; DB 1; Length 197;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 35 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 70

RESULT 5

US-09-288-950-99
; Sequence 99, Application US/09288950
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446C3
; CURRENT APPLICATION NUMBER: US/09/288,950
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-288-950-99

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Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 35 RRVKKGDLKTQVEKLRVFNALKEQALQTVCLR 70

RESULT 6

US-09-346-327-99
; Sequence 99, Application US/09346327
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

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; FILE REFERENCE: 210121.446C4
; CURRENT APPLICATION NUMBER: US/09/346,327
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-346-327-99

    Query Match          90.7%; Score 166; DB 17; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
    Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRVKDKGDLKTQVEKLRWVNALKEMOALQTVCLR 36
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Db 35 RRVKDKGDLKTQIEKLWTEVNALKEIQALQTVCLR 70

RESULT 9
US-09-745-288-99
; Sequence 99, Application US/09745288
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-745-288-99

    Query Match          90.7%; Score 166; DB 21; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
    Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRVKDKGDLKTQVEKLRWVNALKEMOALQTVCLR 36
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Db 35 RRVKDKGDLKTQIEKLWTEVNALKEIQALQTVCLR 70

RESULT 10
US-09-778-381-99
; Sequence 99, Application US/09778381
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C7
; CURRENT APPLICATION NUMBER: US/09/778,381
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-381-99

    Query Match          90.7%; Score 166; DB 21; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
    Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRVKDKGDLKTQVEKLRWVNALKEMOALQTVCLR 36
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Db 35 RRVKDKGDLKTQIEKLWTEVNALKEIQALQTVCLR 70

RESULT 11
US-09-791-537-25686
; Sequence 99, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
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; FILE REFERENCE: 210121.446C4
; CURRENT APPLICATION NUMBER: US/09/346,327
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-346-327-99

    Query Match          90.7%; Score 166; DB 17; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
    Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRVKDKGDLKTQVEKLRWVNALKEMOALQTVCLR 36
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Db 35 RRVKDKGDLKTQIEKLWTEVNALKEIQALQTVCLR 70

RESULT 7
US-09-687-507-99
; Sequence 99, Application US/09687507
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C6
; CURRENT APPLICATION NUMBER: US/09/687,507
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-687-507-99

    Query Match          90.7%; Score 166; DB 20; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
    Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRVKDKGDLKTQVEKLRWVNALKEMOALQTVCLR 36
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Db 35 RRVKDKGDLKTQIEKLWTEVNALKEIQALQTVCLR 70

RESULT 8
US-09-687-507A-99
; Sequence 99, Application US/09687507A
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C6
; CURRENT APPLICATION NUMBER: US/09/687,507A
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-687-507A-99

    Query Match          90.7%; Score 166; DB 20; Length 197;
    Best Local Similarity 86.1%; Pred. No. 1.2e-13;
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; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25686
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-25686

Query Match          90.7%; Score 166; DB 21; Length 197;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 36
Db 35 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 70

RESULT 12
PCT-US02-177-293-55
; Sequence 55, Application US/10177293
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarnu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: PCT-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-55

Query Match          90.7%; Score 166; DB 25; Length 197;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 36
Db 35 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 70

RESULT 13
PCT-US02-12619-2
; Sequence 2, Application PC/TUS0212619
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; FILE REFERENCE: P5024R1-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/12619
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US02-12619-2

Query Match          90.7%; Score 166; DB 1; Length 206;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 36
Db 44 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 79

RESULT 14
PCT-US02-19669-57
; Sequence 57, Application PC/TUS0219669
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669-57

Query Match          90.7%; Score 166; DB 1; Length 206;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 36
Db 44 RRVKKGDLKTOVEKLRREVNALKEQALQTVCLR 79
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Db 44 RVRDKGDLTKQIEKLTVEVNAKLEIQALQTVCLR 79

US-09-709-238-403

RESULT 15

; Sequence 403, Application US/09709238

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Chen, Jian

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Yuan, Jean

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same

; FILE REFERENCE: P2730R1C1

; CURRENT APPLICATION NUMBER: US/09709,238

; CURRENT FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: 1999-06-02

; PRIOR APPLICATION NUMBER: US 60/087,607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,759

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: US 60/087,827

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,025

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,028

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,029

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,030

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,033

; PRIOR FILING DATE: 1998-06-04

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; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,167

; PRIOR FILING DATE: 1988-06-05

; PRIOR APPLICATION NUMBER: US 60/088,202

; PRIOR FILING DATE: 1998-06-05

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; PRIOR APPLICATION NUMBER: US 60/088,217

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: US 60/088,722

; PRIOR FILING DATE: 1998-06-10

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; PRIOR APPLICATION NUMBER: US 60/088,738

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; PRIOR APPLICATION NUMBER: US 60/088,740

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,741

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; PRIOR APPLICATION NUMBER: US 60/088,810

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,811

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,824

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,825

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,826

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,858

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,861

; PRIOR FILING DATE: 1998-06-11

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; PRIOR APPLICATION NUMBER: US 60/088,876

; PRIOR FILING DATE: 1998-06-11

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; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,532

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,538

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,598

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; PRIOR APPLICATION NUMBER: US 60/089,801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,907

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,908

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,947

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/089,948

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; PRIOR APPLICATION NUMBER: US 60/089,952

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/090,246

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,252

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,254

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,355

; PRIOR FILING DATE: 1998-06-23

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; PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-06-23

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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,646
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,673
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/091,982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/092,182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: US 60/092,472
;; PRIOR FILING DATE: 1998-07-10
;; PRIOR APPLICATION NUMBER: US 60/093,339
;; PRIOR FILING DATE: 1998-07-20
;; PRIOR APPLICATION NUMBER: US 60/094,651
;; PRIOR FILING DATE: 1998-07-30

Query Match 90.7%; Score 166; DB 21; Length 206;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRVKKGDKLTQVEKLRFEVNAKEMQALQTVCLR 36
Db 44 RRVKKGDKLTQVEKLRFEVNAKEMQALQTVCLR 79

Search completed: April 15, 2003, 12:04:10
Job time : 186 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:39 ; Search time 23.25 Seconds
(without alignments)
241.276 Million cell updates/sec

Title: US-09-445-576A-38
Perfect score: 183
Sequence: 1 RRVKEDGDKLTQVEKLRVNAKEMQALQTVCLR 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 704857 seqs, 155824263 residues

Total number of hits satisfying chosen parameters: 704857

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2.6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2.6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2.6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2.6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2.6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2.6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2.6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	183	100.0	36	5	US-09-445-576A-38
2	166	90.7	197	1	PCT-US02-19669A-55
3	166	90.7	206	1	PCT-US02-19669A-57
4	166	90.7	206	5	US-09-989-733-403
5	166	90.7	206	5	US-09-992-643-403
6	166	90.7	206	6	US-10-125-923A-276
7	166	90.7	206	6	US-10-205-892-276
8	166	90.7	206	6	US-10-174-575-276
9	166	90.7	206	6	US-10-174-575A-276
10	166	90.7	206	6	US-10-187-755-276
11	166	90.7	206	6	US-10-187-749-276
12	166	90.7	206	6	US-10-199-672-276
13	166	90.7	206	6	US-10-194-486-276
14	124.5	68.0	36	5	US-09-445-576A-39
15	79	43.2	36	5	US-09-445-576A-36
16	79	43.2	52	5	US-09-445-576A-71
17	79	43.2	180	5	US-09-445-576A-27
18	79	43.2	181	5	US-09-445-576A-7
19	79	43.2	197	5	US-09-445-576A-25
20	79	43.2	202	1	PCT-US02-38407-13
21	79	43.2	202	5	US-09-992-095B-62
22	79	43.2	202	5	US-09-999-570-62
23	79	43.2	202	6	US-10-154-678-62
24	79	43.2	202	6	US-10-276-781-1559
25	79	43.2	228	5	US-09-445-576A-24
26	77	42.1	51	5	US-09-445-576A-35

27	76	41.5	36	5	US-09-445-576A-37	Sequence 37, Appl
28	69	37.7	52	5	US-09-445-576A-5	Sequence 5, Appl1
29	69	37.7	73	5	US-09-445-576A-28	Sequence 28, Appl
30	64	35.0	49	5	US-09-445-576A-6	Sequence 6, Appl1
31	64	35.0	65	5	US-09-445-576A-26	Sequence 26, Appl
32	62	33.9	36	5	US-09-445-576A-40	Sequence 40, Appl
33	60	32.8	69	5	US-09-445-576A-29	Sequence 29, Appl
34	60	32.8	145	5	US-09-445-576A-31	Sequence 31, Appl
35	60	32.8	330	5	US-09-445-576A-32	Sequence 32, Appl
36	60	32.8	331	5	US-09-445-576A-33	Sequence 33, Appl
37	60	32.8	592	5	US-09-445-576A-34	Sequence 34, Appl
38	58	31.7	459	5	US-09-724-676-64184	Sequence 64184, A
39	58	31.7	459	5	US-09-724-676A-64184	Sequence 64184, A
40	58	31.7	565	5	US-09-949-016-7293	Sequence 7293, Ap
41	57.5	31.4	369	6	US-10-126-052A-421	Sequence 421, App
42	57	31.1	209	7	US-60-452-680-14638	Sequence 14638, A
43	57	31.1	209	7	US-60-453-135-9127	Sequence 9127, Ap
44	57	31.1	209	7	US-60-453-050-9127	Sequence 9127, Ap
45	57	31.1	474	6	US-10-094-749-3090	Sequence 3090, Ap

ALIGNMENTS

RESULT 1
US-09-445-576A-38
; Sequence 38, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreen Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bovine
US-09-445-576A-38

Query Match 100.0%; Score 183; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9,4e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RRVKEKDGLKTQVEKLRVNAKEMQALQTVCLR	36
Db	1	RRVKEKDGLKTQVEKLRVNAKEMQALQTVCLR	36

RESULT 2
PCT-US02-19669A-55
; Sequence 55, Application PC/TUS0219669A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
; OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506


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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/992,643
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 403
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-643-403

Query Match          90.7%; Score 166; DB 5; Length 206;
Best Local Similarity 86.1%; Pred. No. 2.5e-16;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKRDGDLKTQVEKLRVFNALKEQALQTVCLR 36
   |||:|||||:|||||:|||||:|||||:|||||
Db 44 RRVKRDGDLKTQVEKLRVFNALKEQALQTVCLR 79

RESULT 6
US-10-125-923A-276
; Sequence 276, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/05263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-923A-276

Query Match          90.7%; Score 166; DB 6; Length 206;
Best Local Similarity 86.1%; Pred. No. 2.5e-16;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKRDGDLKTQVEKLRVFNALKEQALQTVCLR 36
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Db 44 RRVKRDGDLKTQVEKLRVFNALKEQALQTVCLR 79

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US-10-205-892-276
; Sequence 276, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C517
; CURRENT APPLICATION NUMBER: US/10/205,892
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052536
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
```

us-09-445-576a-38.rapn

[illegible]

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC1
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/187,755
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
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; PRIOR APPLICATION NUMBER: 60/063121
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; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-276

Query Match          90.7%; Score 166; DB 6; Length 206;
Best Local Similarity 86.1%; Pred. No. 2.5e-16;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKEDGDLKTQVEKLRWREVNALKEMQALQTVCLR 36
    |||:|||||:|||||:|||||:|||||:|||||:
Db 44 RVRDKDGLKTQIEKLRWTEVNALKETQALQTVCLR 79

RESULT 11
US-10-187-749-276
; Sequence 276, Application US/10187749
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC1
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/187,749
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
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; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-755-276

Query Match          90.7%; Score 166; DB 6; Length 206;
Best Local Similarity 86.1%; Pred. No. 2.5e-16;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKEDGDLKTQVEKLRWREVNALKEMQALQTVCLR 36
    |||:|||||:|||||:|||||:|||||:|||||:
Db 44 RVRDKDGLKTQIEKLRWTEVNALKETQALQTVCLR 79

RESULT 11
US-10-187-749-276
; Sequence 276, Application US/10187749
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC1
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/187,749
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
```

```
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-276

Query Match          90.7%; Score 166; DB 6; Length 206;
Best Local Similarity 86.1%; Pred. No. 2.5e-16;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKEDGDLKTQVEKLRWREVNALKEMQALQTVCLR 36
    |||:|||||:|||||:|||||:|||||:|||||:
Db 44 RVRDKDGLKTQIEKLRWTEVNALKETQALQTVCLR 79

RESULT 12
US-10-199-672-276
; Sequence 276, Application US/10199672
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC1
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-276
```


Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	124.5	68.0	166	1	A37289	tetranectin homolo
2	79	43.2	202	1	TTHUN	tetranectin precur
3	76	41.5	202	2	JC4031	tetranectin precu
4	65	35.5	630	2	T38023	probable transcrip
5	61	33.3	1008	2	H72310	conserved hypothet
6	59	32.2	251	2	G97579	ABC transporter At
7	59	32.2	251	2	AE2800	hypothetical prote
8	58	31.7	517	2	B40583	heat shock transcr
9	58	31.7	536	2	A41138	heat shock transcr
10	58	31.7	631	2	D90551	lipoprotein limpor
11	57.5	31.4	1844	2	T51890	related to Nup98-N
12	56.5	30.9	1017	2	PC4035	cell-cycle-depende
13	56	30.6	73	2	D69104	conserved hypothet
14	55.5	30.3	1265	2	T47626	structural mainten
15	55	30.1	156	2	D83769	hypothetical prote
16	55	30.1	306	1	G69002	conserved hypothet
17	55	30.1	391	2	AB0443	hypothetical prote
18	54.5	29.8	659	2	T34142	hypothetical prote
19	54.5	29.8	759	2	F64662	trans-Golgi membra
20	54	29.5	102	2	S57536	hypothetical prote
21	54	29.5	319	2	T01546	hypothetical prote
22	54	29.5	862	2	T01798	hypothetical prote
23	54	29.5	976	2	G84587	hypothetical prote
24	54	29.5	1011	2	T17430	tol protein - Neur
25	53.5	29.2	952	2	T50451	hypothetical coile
26	53	29.0	520	2	G84868	hypothetical prote
27	52.5	28.7	989	2	T48845	insulin II gene en
28	52	28.4	325	2	E84045	acetyl-CoA carboxy
29	52	28.4	489	2	S05474	keratin 8, type II

```

Biochemistry 26, 6757-6764, 1987
A:Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protein
A:Reference number: A29747; MUID:88107595; PMID:3427041
A:Accession: A29747
A:Molecule type: protein
A:Residues: 22-105, 'G', 107-202 <FUH>
A:Experimental source: plasma
A:Note: 55-Ser and 58-Met were also found
C:Genetics:
A:Gene: GDB:TNA
A:Cross-references: GDB:135032; OMIM:187520
A:Map position: 3p22-3p21.3
A:Introns: 37/1; 70/1
C:Complex: homotetramer
C:Superfamily: tetranectin; C-type lectin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-202/Product: tetranectin #status experimental <MAT>
F:71-197/Domain: C-type lectin homology <LCH>
F:25/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:71-81, 98-197, 173-189/Disulfide bonds: #status experimental

Query Match 43.2%; Score 79; DB 1; Length 202;
Best Local Similarity 57.1%; Pred. No. 0.013;
Matches 16; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 9 DLKTOVEKLRVNAKEMQALQTVCLR 36
Db 46 ELKSRDLTQAEVALLKEQQALQTVCLK 73

RESULT 3
JC4031
tetranectin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C:Accession: JC4031
Gene 152, 243-245, 1995
A:Title: Cloning of a cDNA encoding murine tetranectin.
A:Reference number: JC4031; MUID:95137396; PMID:7835708
A:Accession: JC4031
A:Molecule type: mRNA
A:Residues: 1-202 <SOR>
A:Cross-references: EMBL:X79199; NID:9671561; PIDN:CAA55791.1; PID:9671562
A:Experimental source: lung
A:Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C:Superfamily: tetranectin; C-type lectin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-202/Product: tetranectin #status predicted <MAT>
F:71-197/Domain: C-type lectin homology <LCH>

Query Match 41.5%; Score 76; DB 2; Length 202;
Best Local Similarity 57.1%; Pred. No. 0.031;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 9 DLKTOVEKLRVNAKEMQALQTVCLR 36
Db 46 ELKSRDLTQAEVALLKEQQALQTVCLK 73

RESULT 4
T38023
probable transcription regulator - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C:Accession: T38023
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21763
A:Accession: T38023
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

```

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A:Residues: 1-630 <MUR>
A:Cross-references: EMBL:Z98598; PIDN:CAB11234.1; GSPDB:GN00066; SPDB:SPAC1B3.05
A:Experimental source: strain 972h; cosmid c1B3
C:Genetics:
A:Gene: SPDB:SPAC1B3.05
A:Map position: 1
A:Introns: 75/3

```

```

Query Match 35.5%; Score 65; DB 2; Length 630;
Best Local Similarity 43.2%; Pred. No. 2.4;
Matches 16; Conservative 6; Mismatches 10; Gaps 2;

```

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Qy 4 KEK-DGDLKTQVEKL-----WREYNALKEMQAL 30
Db 30 KEKLEGLDKTQIKLQRLRDLQIKTWASSNDIKKKAL 66

```

RESULT 5

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H72310
conserved hypothetical protein - Thermotoga maritima (strain MSB8)

```

```

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72310
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic-
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

```

```

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72310
A:Status: preliminary
A:Molecule type: DNA

```

```

A:Residues: 1-1008 <ARN>
A:Cross-references: GB:AE001760; GB:AE000512; NID:94981510; PIDN:AAD36066.1; PID:9498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0987
C:Superfamily: conserved hypothetical protein PH0905

```

```

Query Match 33.3%; Score 61; DB 2; Length 1008;
Best Local Similarity 43.8%; Pred. No. 13;
Matches 14; Conservative 4; Mismatches 8; Indels 6; Gaps 1;

```

```

Qy 2 RVKEKDGDL-----KTQVEKLRVNAKREM 27
Db 344 KVKVKGDLTFEPATKEDSEKLRKAKKVRREM 375

```

RESULT 6

```

G97579
ABC transporter ATP-binding protein XF1475 [imported] - Agrobacterium tumefaciens (st
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: G97579
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldm

```

```

Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: G97579
A:Status: preliminary
A:Molecule type: DNA

```

```

A:Residues: 1-251 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK87592.1; PID:g15156934; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_3346
A:Map position: circular chromosome
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

```

```

Query Match 32.2%; Score 59; DB 2; Length 251;
Best Local Similarity 41.5%; Pred. No. 5.3;
Matches 17; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

```


A:Introns: 34/1; 1281/3

Query Match 31.4%; Score 57.5; DB 2; Length 1844;
Best Local Similarity 63.2%; Pred. No. 66;
Matches 12; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 9 DLKTOVEKLRWREVNALKEM 27

DB 1442 DLKTLQDD-WREANVLSE 1459

RESULT 12

PC4035

cell-cycle-dependent 350K nuclear protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C:Accession: PC4035

R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.

Biochem. Biophys. Res. Commun. 212, 220-228, 1995

A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient

A:Reference number: PC4035; MUID:95336446; PMID:7612011

A:Accession: PC4035

A:Molecule type: DNA

A:Residues: 1-1017 <LIQ>

A:Cross-references: GB:U25725; NID:9818866; PIDN:AAA6889.1; PID:9818867

A:Note: repeat 15-160 and 200-340

C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-terminus

C:Keywords: nucleoprotein; phosphoprotein

F:465/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #stat

F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #statu

F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status p

Query Match

Best Local Similarity 30.98; Score 56.5; DB 2; Length 1017;

Matches 14; Conservative 7; Mismatches 8; Indels 3; Gaps 1;

QY 2 RVKEKDG- --LKTQVEKLRWREVNALKEMQAL 30

DB 44 KLKERDGENSLKDKVENLERELQMSBNQEL 75

RESULT 13

D69104

conserved hypothetical protein MTH1778 - Methanobacterium thermoautotrophicum (strain De

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: D69104

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: D69104

A:Molecule type: DNA

A:Residues: 1-73 <MTH>

A:Cross-references: GB:AE000933; GB:AE000666; NID:g2622908; PIDN:AAB86244.1; PID:g262290

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1778

A:Start codon: GTG

Query Match

Best Local Similarity 30.6%; Score 56; DB 2; Length 73;

Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRVKERDGLKTOVEKLRWREVNALKEM 27

DB 43 REVHERIGIERGIEDLRREVAEIKEM 69

RESULT 14

PC4035

cell-cycle-dependent 350K nuclear protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C:Accession: PC4035

R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.

Biochem. Biophys. Res. Commun. 212, 220-228, 1995

A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient

A:Reference number: PC4035; MUID:95336446; PMID:7612011

A:Accession: PC4035

A:Molecule type: DNA

A:Residues: 1-1017 <LIQ>

A:Cross-references: GB:U25725; NID:9818866; PIDN:AAA6889.1; PID:9818867

A:Note: repeat 15-160 and 200-340

C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-terminus

C:Keywords: nucleoprotein; phosphoprotein

F:465/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #stat

F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #statu

F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status p

T47626

structural maintenance of chromosomes (SMC)-like protein - Arabidopsis thaliana

N:Alternate names: protein T5N23.30

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47626

R:Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeltner, K.; Mewes, H.W.; Lemcke, K.

submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24463

A:Accession: T47626

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1265 <OBE>

A:Cross-references: EMBL:AL138650

A:Experimental source: cultivar Columbia; BAC clone T5N23

C:Genetics:

A:Map position: 3

A:Introns: 147/3; 226/3; 312/3; 392/2; 481/2; 571/3; 620/3; 670/1; 706/1; 752/3; 784/

A:Note: T5N23.30

Query Match

Best Local Similarity 30.3%; Score 55.5; DB 2; Length 1265;

Matches 12; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 RRVKEKDGDLKTOVEKLRWREVNALK-EMQALQ 31

DB 443 KRFXDRQGEITSSSKYKNETTSLKTELRLAQ 474

RESULT 15

D83769

hypothetical protein BH0956 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: D83769

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: D83769

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-156 <STO>

A:Cross-references: GB:AP001510; GB:BA000004; NID:gl0173440; PIDN:BA04675.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0956

Query Match

Best Local Similarity 30.1%; Score 55; DB 2; Length 156;

Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 KGDGLKTOVEKLRWREVNALK 25

DB 2 KNIELASKIDKLWRETKACK 21

Search completed: April 15, 2003, 11:51:07

Job time: 14.75 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:44:09 ; Search time 6.5 Seconds
(without alignments)
229.715 Million cell updates/sec

Title: US-09-445-576A-38

Perfect score: 183

Sequence: 1 RRVKEKDGDLTKQVEKLWREVNALKEMOALQTVCLR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	166	90.7	197	1 CLFL_HUMAN	O75596 homo sapien
2	124.5	68.0	166	1 TETN_CARSP	P26258 carcharhinu
3	79	43.2	202	1 TETN_HUMAN	P05452 homo sapien
4	76	41.5	202	1 TETN_MOUSE	P43025 mus musculu
5	58	31.7	517	1 HSF2_MOUSE	P38533 mus musculu
6	58	31.7	536	1 HSF2_HUMAN	Q03933 homo sapien
7	54	29.5	102	1 YNI6_YEAST	P48232 saccharomyc
8	52.5	28.7	989	1 SMB2_MESAU	Q60560 mesocricetu
9	52	28.4	488	1 KZC8_MOUSE	P11679 mus musculu
10	51	27.9	131	1 MCRD_METFE	P12974 methanother
11	51	27.9	235	1 RR2_GUITH	O78482 guillardia
12	51	27.9	358	1 PTPA_HUMAN	O15257 homo sapien
13	51	27.9	446	1 MUC_CHICK	P01875 gallus gall
14	51	27.9	472	1 CRTI_SYNY3	P29273 synechocyst
15	51	27.9	875	1 IMBI_RAT	P52296 rattus norv
16	51	27.9	1509	1 MYSN_ACACA	P05659 acanthamoeb
17	50.5	27.6	223	1 SODM_ONCOC	P41981 onchocerca
18	50.5	27.6	1610	1 CCAD_MESAU	Q99244 mesocricetu
19	50.5	27.6	2161	1 CCAD_HUMAN	Q01668 homo sapien
20	50.5	27.6	2203	1 CCAD_RAT	P27732 rattus norv
21	50	27.3	206	1 KGUA_HELPJ	Q9zmb7 helicobacte
22	50	27.3	206	1 KGUA_HELPY	P56103 helicobacte
23	50	27.3	251	1 SODE_MOUSE	O09164 mus musculu
24	50	27.3	434	1 SEP6_HUMAN	Q14141 homo sapien
25	50	27.3	434	1 SEP6_MOUSE	Q9rlt4 mus musculu
26	50	27.3	491	1 HSF1_CHICK	P38529 gallus gall
27	50	27.3	503	1 HSF1_MOUSE	P38532 mus musculu
28	50	27.3	529	1 HSF1_HUMAN	Q00613 homo sapien
29	50	27.3	626	1 PEPO_LACLA	O07744 lactococcus
30	50	27.3	626	1 PEPO_LACLC	Q09145 lactococcus
31	50	27.3	867	1 RRPO_BYDVP	P09505 barley yell
32	49.5	27.0	81	1 YIIU_ECOLI	P32164 escherichia
33	49.5	27.0	156	1 MAFK_CHICK	Q90596 gallus gall

RESULT 1

ID	CLFL_HUMAN	STANDARD	PRT	197 AA
AC	O75596			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-type lectin superfamily member 1 precursor (Cartilage-derived C-type lectin).			
DE	CLCFSF1			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cartilage;			
RX	MEDLINE=99453719; PubMed=10524194;			
RA	Neame P.J., Tapp H., Grimm D.R.;			
RT	"The cartilage-derived, C-type lectin (CLECSF1): structure of the gene and chromosomal location."			
RL	Biochim. Biophys. Acta 146:193-202(1999).			
CC	-1- TISSUE SPECIFICITY: Restricted to cartilage.			
CC	-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL; AF077345; AAD12542.1;			
DR	EMBL; AF077344; AAD12542.1; JOINED.			
DR	HSSP; P05452; 1HTN.			
DR	GeneW; HGNC:2052; CLECSF1.			
DR	InterPro; IPR001304; Lectin_C.			
DR	Pfam; PF00059; Lectin_c; 1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C-TYPE_LECTIN_1; 1.			
DR	PROSITE; PS50041; C-TYPE_LECTIN_2; 1.			
KW	Lectin; Signal.			
FT	SIGNAL 1 22 POTENTIAL.			
FT	CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.			
FT	DOMAIN 74 192 C-TYPE LECTIN.			
FT	DISULFID 68 78 BY SIMILARITY.			
FT	DISULFID 95 191 BY SIMILARITY.			
FT	DISULFID 167 183 BY SIMILARITY.			
SQ	SEQUENCE 197 AA; 22232 MW; BB924DBDBB7729A4 CRC64;			
Query Match 90.7%; Score 166; DB 1; Length 197;				
Best Local Similarity 86.1%; Pred. No. 3.3e-14;				
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;				
Oy	1 RRVKEKDGDLTKQVEKLWREVNALKEMOALQTVCLR	36		


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DR PIR: S24126; S24126.
DR PDB: 1HTN; 03-DEC-97.
DR PDB: 1TN3; 06-MAY-98.
DR Genew: HGNC:11891; TNA.
DR MIN: 187520; -.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 202
FT DOMAIN 77 198
FT DISULFID 71 81
FT DISULFID 98 197
FT DISULFID 173 189
FT CARBOHYD 25 25
FT VARIANT 55 55
FT VARIANT 58 58
FT VARIANT 106 106
FT VARIANT 106 106
FT SEQUENCE 202 AA; 22567 MW; 2B0DCB5DF22E1AB8 CRC64;

Query Match 43.2%; Score 79; DB 1; Length 202;
Best Local Similarity 57.1%; Pred. No. 0.004;
Matches 16; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 9 DLKTOVKLWREVNALKEMQALQTVCLR 36
Db 46 ELKSRDLTLAQEVALLEKQALQTVCLK 73

RESULT 4
TETN_MOUSE
ID TETN_MOUSE STANDARD; PRT; 202 AA.
AC P43025;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=95137396; PubMed=7835708;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of a cDNA encoding murine tetranectin.";
RL Gene 152:243-245(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=96116955; PubMed=8563165;
RA Ibaraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.;
RT "Mouse tetranectin: cDNA sequence, tissue-specific expression, and
chromosomal mapping.";
RL Mann. Genome 6:693-696(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=98072445; PubMed=9409787;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of the murine tetranectin gene and 5'-flanking region.";
RL Gene 201:199-202(1997).
CC -!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules, destined for
CC exocytosis (By similarity).
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CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-----
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CC EMBL: X79199; CAA55791.1; -.
CC EMBL: U08595; AAA96811.1; -.
CC EMBL: X98122; CAA66804.1; -.
CC HSP: P05452; ITN3.
CC MGD: MGI:104540; Tna.
CC InterPro: IPR001304; Lectin_C.
CC Pfam: PF00059; lectin_c; 1.
CC SMART: SM00034; CLECT; 1.
CC PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Plasma; Signal.
FT SIGNAL 1 21
FT CHAIN 22 202
FT DOMAIN 77 198
FT DISULFID 71 81
FT DISULFID 98 197
FT DISULFID 173 189
FT CONFLICT 19 20
FT CONFLICT 84 84
FT CONFLICT 180 180
FT CONFLICT 188 188
FT SEQUENCE 202 AA; 22257 MW; 639E7334D58EB04E CRC64;

Query Match 41.5%; Score 76; DB 1; Length 202;
Best Local Similarity 57.1%; Pred. No. 0.0096;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 9 DLKTOVKLWREVNALKEMQALQTVCLR 36
Db 46 ELKSRDLTLAQEVALLEKQALQTVCLK 73

RESULT 5
HSF2_MOUSE
ID HSF2_MOUSE STANDARD; PRT; 517 AA.
AC P38533;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor
DE 2) (HSTF 2).
GN HSF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RX MEDLINE=92009180; PubMed=1717345;
RA Sarge K.D., Zimarino V., Holm K., Wu C., Morimoto R.I.;
RT "Cloning and characterization of two mouse heat shock factors with
RT distinct inducible and constitutive DNA-binding ability.";
RL Genes Dev. 5:1902-1911(1991).
CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER
CC EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
CC HEAT SHOCKED. HSF2 IS EXPRESSED IN A FORM THAT BINDS DNA
CC CONSTITUTIVELY BUT LOSES DNA BINDING BY INCUBATION AT GREATER THAN
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CC 41 DEGREES C.
CC -1- SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
CC OTHERWISE FOUND AS A HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
CC TO THE NUCLEUS UPON ACTIVATION.
CC -1- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC -----
CC EMBL; X61754; CAA43893.1; -
CC PIR; B40583; B40583.
CC HSSP; P22121; 2HTS.
CC TRANSFAC; T00972; -
CC MGD; MGI:96239; Hsf2.
CC InterPro; IPR000232; HSF_DNA_bind.
CC Pfam; PF00447; HSF_DNA-bind; 1.
CC PRINTS; PR00056; HSFDOMAIN.
CC ProDom; PD001788; HSF_DNA_bind; 1.
CC SMART; SM00415; HSF; 1.
CC PROSITE; PS00434; HSF_DOMAIN; 1.
CC Transcription regulation; Nuclear protein; DNA-binding; Activator;
KW Phosphorylation; Heat shock; Multigene family.
FT DOMAIN 7 112 BY SIMILARITY.
FT DOMAIN 119 192 HYDROPHOBIC REPEAT HR-A/B.
FT DOMAIN 359 384 HYDROPHOBIC REPEAT HR-C.
FT SEQUENCE 517 AA; 58155 MW; 098965BBCDF4E1B0 CRC64;

Query Match 31.7%; Score 58; DB 1; Length 517;
Best Local Similarity 32.4%; Pred. No. 5.2;
Matches 11; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 3 VKEKGDGLKQVEKLRVNAKEMQALQTVCLR 36
DB 143 IESRLSELKSESLWKEVSELRAKHAQQQVIR 176
::: |||: | |||: | | | | |

RESULT 6
HSF2_HUMAN STANDARD; PRT; 536 AA.
AC Q03933;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor
DE 2) (HSF 2).
GN HSF2 OR HSF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 65-71.
RX MEDLINE=91334377; PubMed=1871106;
RA Schuetz T.J., Gallo G.J., Sheldon L., Tempst P., Kingston R.E.;
RT "Isolation of a cDNA for HSF2: evidence for two heat shock factor
RT genes in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:6911-6915(1991).
RN [2]
RP SUBCELLULAR LOCATION, AND MUTAGENESIS.
RX MEDLINE=93339580; PubMed=8339932;
RA Sheldon L., Kingston R.E.;
RT "Hydrophobic coiled-coil domains regulate the subcellular
RT localization of human heat shock factor 2.";
RL Genes Dev. 7:1549-1558(1993).
CC -1- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER

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CC EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
CC HEAT SHOCKED.
CC -1- SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
CC OTHERWISE FOUND AS A HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
CC TO THE NUCLEUS UPON ACTIVATION.
CC -1- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC -----
CC EMBL; M65217; AAA36017.1; -
CC PIR; A41138; A41138.
CC HSSP; P22813; 1HK7.
CC TRANSFAC; T01043; -
CC Genew; HGNC:5225; HSF2.
CC MIM; 140581; -
CC InterPro; IPR000232; HSF_DNA_bind.
CC InterPro; IPR002341; HSF_ETS.
CC Pfam; PF00447; HSF_DNA-bind; 1.
CC PRINTS; PR00056; HSFDOMAIN.
CC ProDom; PD001788; HSF_DNA_bind; 1.
CC SMART; SM00415; HSF; 1.
CC PROSITE; PS00434; HSF_DOMAIN; 1.
CC Transcription regulation; Nuclear protein; DNA-binding; Activator;
KW Phosphorylation; Heat shock; Multigene family.
FT DOMAIN 7 112 BY SIMILARITY.
FT DOMAIN 119 192 HYDROPHOBIC REPEAT HR-A/B.
FT DOMAIN 360 385 HYDROPHOBIC REPEAT HR-C.
FT DOMAIN 108 122 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 195 210 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 170 173 POLY-GLN.
FT MUTAGEN R->G; FAIL TO TRANSLOCATE TO NUCLEUS.
FT MUTAGEN 196 198 RKR->ASS; FAIL TO TRANSLOCATE TO NUCLEUS.
FT SEQUENCE 536 AA; 60348 MW; 00DFD05CFD9DF0D3 CRC64;

Query Match 31.7%; Score 58; DB 1; Length 536;
Best Local Similarity 32.4%; Pred. No. 5.4;
Matches 11; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 3 VKEKGDGLKQVEKLRVNAKEMQALQTVCLR 36
DB 143 IESRLSELKSESLWKEVSELRAKHAQQQVIR 176
::: |||: | |||: | | | | |

RESULT 7
YNI6_YEAST STANDARD; PRT; 102 AA.
AC P48232;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 11.5 kDa protein in TOP2-MKT1 intergenic region.
GN YNL086W OR N2254.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FV1679;
RX MEDLINE=96310628; PubMed=8740422;
RA Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M.;
RT "The sequence of a 17,933 bp segment of Saccharomyces cerevisiae
RT chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and five
RT new open reading frames.";
RL Yeast 12:485-491(1996).

```


FT	DOMAIN	860	864	NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
SQ	SEQUENCE	989 AA:	108439 MW;	9489671E46DAD04E CRC64;

Query Match	28.7%	Score 52.5;	DB 1;	Length 989;
Best Local Similarity	35.5%	Pred. No. 52;		

QY 5 EKDGDLKTOVEKLRREVNALKEMQALQTVCL 35
 matches 11; conservative 10; mismatches 9; indels 1; gaps 1

RESULT 9

18 ELEKDAEVEERKSNQEHSSLNELQS-RGVCL 4 /

ID	R2C6_MOUSE	PK1;	400 AA.
AC	P11679;	STANDARD;	
DT	01-OCT-1989	(Rel. 12, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	

DE Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A).
 GN KRT8 OR KRT2-8.
 OS *Mus musculus* (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RX MEDLINE=88255624; PubMed=2454862;
RA Senat A., Vasseur M., Maillet L., Brulet P., Darmon Y.M.;

RT Evidence for mRNA species initiated upstream of the normal 5' end in
RT PCC4 cells.";
RL Differentiation 37:40-46(1988).

SEQUENCE FROM N.A.
RP
RX MEDLINE=89121483; PubMed=2464527;
RA Morita T., Tondella M.L.C., Takemoto Y., Hashido K., Ichinose Y.,

RT "Nucleotide sequence of mouse EndoA cytoke-
RT RT polypeptide characteristics of the type-II keratin subfamily.";
RL Gene 68:109-117(1988).

CC -1- SUBUNIT; HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
CC KERATIN 8 ASSOCIATES WITH KERATIN 18.
CC MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
CC MICROFIBILLAR KERATIN I (ACIDIC) AND II (NEUTRAL TO BASIC)

CC (40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
CC
CC -|- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC -----
CC

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 CC -----

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DR EMBL; X15662; CAA33697.1; -
DR EMBL; M21836; AAA37550.1; -
DR EMBL; M21836; AAA37551.1; ALT_INIT.
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DR FLN; S03474; S03474.
DR SWISS-2DPAGE; P11679; MOUSE.
DR MGD; MGI:96705; Krt2-8.
DR InterPro: IPR001664; IF.

DR InterPro; IPR003054; Keratin_11.

KW	Helicase; ATP-binding; DNA-binding; Nuclear protein;
KW	Transcription regulation; Activator.
PT	NP BIND 213 220 ATP-(POTENTIAL).

FT	DOMAIN	250	425	LEQ-RICH.
FT	DOMAIN	370	373	POLY-VAL.
FT	DNA_BIND	637	783	SS DNA-BINDING (BY SIMILARITY).
FT	DOMAIN	793	859	GIN/PRO-RICH

	860	864	POLY-LYS.
FT DOMAIN	860	864	NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN	860	864	
SQ SEQUENCE	989 AA;	108439 MW;	9489671E46DAD04E CRC64;

Query Match 28.7%; Score 52.5; DB 1; Length 989;
Best Local Similarity 35.5%; Pred. No. 52;
Matches 11; Conservative 10; Mismatches 9; Indels 1; Gaps

Qy 5 ERDGDLTQVEKLNREVNALKEMQALQTVCL 35
 | : | : : : | : ||| : : |||
Dd 18 ELERDAEVEFRSSQEHSLKELQS-RGVCL 47

RESULT 9
K2C8_MOUSE

DT	01-NOV-1997	(Rel. 35, Last sequence update)
DT	01-OCT-1989	(Rel. 12, Created)
AC	P11679;	
AC	REC00002	SRIMAND, 191, 400 Mi.

DE Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A).
GN KRT8 OR KRT2-8.
OS *Mus musculus* (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
EN 11

RP SEQUENCE FROM N.A.
RX MEDLINE=88255624; PubMed=2454862;
RA Senat A., Vasseur M., Maillet L., Brulet P., Darmon Y.M.;
RM "Genotype analysis of multiple autoantibodies in type 1 diabetes mellitus: a study of 95 patients with type 1 diabetes mellitus and 95 healthy controls." *Diabetes* 1998;47:100-105. PMID: 9500000

RT Evidence for mRNA species initiated upstream of the normal 5' end in
RT PCC4 cells.";
RL Differentiation 37:40-46(1988).

RP SEQUENCE FROM N.A.
RX MEDLINE=89121483; PubMed=2464527;
RA Morita T., Tondella M.L.C., Takemoto Y., Hashido K., Ichinose Y.,

RT "Nucleotide sequence of mouse EndoA cytokeratin cDNA reveals
RT polypeptide characteristics of the type-II keratin subfamily.";
RL Gene 68:109-117(1988).

CC -I- SUBUNIT: HETERODIMER OF TWO TYPE I AND TWO TYPE II KERATINS.
CC KERATIN 8 ASSOCIATES WITH KERATIN 18.
CC -I- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
CC MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)

CC (40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
CC
CC -|- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC
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DR ENBL; X15662; CAA33697.1; -.
DR ENBL; M21836; AAA37550.1; -.
DR ENBL; M21836; AAA37551.1; ALT_INIT.
```

DR SWISS-2DPAGE; P11679; MOUSE.
DR MGD; MGI:96705; Krt2-8.
DR InterPro; IPR001664; IF.

DR INCEP10; IPR003034; KEGG11_11.

```

DR Pfam: PF00038; filament; 1.
DR PRINTS: PR01276; TYPEKERATIN.
DR PROSITE: PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Keratin; Phosphorylation.
FT INT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 95 HEAD.
FT DOMAIN 96 402 ROD.
FT DOMAIN 403 488 TAIL.
FT DOMAIN 96 131 COIL 1A.
FT DOMAIN 132 148 LINKER 1.
FT DOMAIN 149 240 COIL 1B.
FT DOMAIN 241 264 LINKER 12.
FT DOMAIN 265 402 COIL 2.
FT SITE 346 346 STUTTER.
FT MOD_RES 23 23 PHOSPHORYLATION (BY MAPK AND CAMK2) (BY
FT MOD_RES 436 436 PHOSPHORYLATION (BY MAPK AND CAMK2) (BY
FT SIMILARITY)
FT CONFLICT 189 190 QQ -> NR (IN REF. 2).
FT CONFLICT 324 324 E -> EA (IN REF. 2).
FT CONFLICT 366 366 P -> R (IN REF. 2).
SQ SEQUENCE 488 AA; 54318 MW; 9E1430800B81523 CRC64;

Query Match 28.4%; Score 52; DB 1; Length 488;
Best Local Similarity 36.7%; Pred. No. 28;
Matches 11; Conservative 9; Mismatches 6; Indels 4; Gaps 1;

QY 6 KQGD-----LKTQVEKLMREYNALKEMQALQ 31
DB 300 KHGDLRLRTKTEISEMNRNRLQETALK 329

RESULT 10
MCRD_METFE STANDARD; PRT; 131 AA.
AC P12974;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase operon protein D.
GN MCRD.
OS Methanothermobacter fervidus.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanothermobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=2180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89008091; PubMed=3170483;
RA Weil C.F., Cram D.S., Sherf B.A., Reeve J.N.;
RT "Structure and comparative analysis of the genes encoding component C
RT of methyl coenzyme M reductase in the extremely thermophilic
RT archaeobacterium Methanothermobacter fervidus.";
RL J. Bacteriol. 170:4718-4726(1988).
CC -1- PATHWAY: Methanogenesis; last step.
CC -1- SUBUNIT: MCR IS COMPOSED OF THREE SUBUNITS: ALPHA, BETA, AND
CC GAMMA. THE FUNCTION OF PROTEINS C AND D IS NOT KNOWN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03375; AA72194.1; -
DR InterPro: IPR003901; MthCOMR_D.
DR Pfam: PF02505; MCR_D; 1.
KW Methanogenesis.
SQ SEQUENCE 131 AA; 15086 MW; B7C6F746AB0C98AF CRC64;

Query Match 27.9%; Score 51; DB 1; Length 131;
Best Local Similarity 31.2%; Pred. No. 9;
Matches 10; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

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```

QY 3 VKKDGDLKTQVEKLMREYNALKEMQALQTV 34
DB 52 VKGQDIELKVKTGRIEVEIEDKKTMEKIREVC 83

RESULT 11
RR2_GUITH STANDARD; PRT; 235 AA.
AC O78482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Chloroplast 30S ribosomal protein S2.
GN RPS2.
OS Guillardia theta (Cryptomonas phi).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=99299392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved syntenic groups confirm its common
RT ancestry with red algae.";
RL J. Mol. Evol. 48:236-244(1999).
CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF041468; AAC35673.1; -
DR InterPro: IPR001865; Ribosomal_S2.
DR Pfam: PF00318; Ribosomal_S2; 1.
DR PRINTS: PR00395; RIBOSOMAL_S2.
DR TIGRFAMs: TIGR01011; rpsB_bact; 1.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE: PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Chloroplast.
SQ SEQUENCE 235 AA; 26712 MW; 1360A0A1368A6A93 CRC64;

Query Match 27.9%; Score 51; DB 1; Length 235;
Best Local Similarity 37.0%; Pred. No. 17;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 4 KEKDGDLKTQVEKLMREYNALKEMQAL 30
DB 130 KKEAGLRRELEKLRNLGNLKNMKRL 156

RESULT 12
PTPA_HUMAN STANDARD; PRT; 358 AA.
AC Q15257; Q15258; Q9BUK1; Q9NNZ7; Q9NNZ8; Q9NNZ9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53
DE isoform) (Phosphotyrosyl phosphatase activator) (PTPA).
GN PPP2R4 OR PTPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM 1).
RC TISSUE=Heart;

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DR PIR: A02170; MHCH.
 DR HSP: P01857; IFC1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig-like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00410; Ig-like; 2.
 DR SMART: SM00407; IGL1; 1.
 DR SMART: PS00290; Ig_MHC; 3.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 105 CH1.
 FT DOMAIN 106 209 CH2.
 FT DOMAIN 210 316 CH3.
 FT DOMAIN 317 427 CH4.
 FT DOMAIN 428 446
 FT DISULFID 16 16
 FT FT
 FT DISULFID 27 85
 FT DISULFID 135 190
 FT DISULFID 237 296
 FT DISULFID 284 284
 FT FT
 FT DISULFID 344 406
 FT DISULFID 445 445
 FT FT
 FT CARBOHYD 45 45
 FT CARBOHYD 46 46
 FT CARBOHYD 73 73
 FT CARBOHYD 130 130
 FT CARBOHYD 198 198
 FT CARBOHYD 382 382
 FT CARBOHYD 433 433
 FT CARBOHYD 446 446
 FT SEQUENCE 446 AA; 48173 MW; 3CB0CE108949BD17 CRC64;
 Query Match 27.9%; Score 51; DB 1; Length 446;
 Best Local Similarity 38.7%; Pred. No. 34;
 Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
 OY 4 KEKDGDKTQVEKLRVNAKEMQALQTV 34
 DB 254 KEKGGKLETALGKRVQLQSLVTDGVATVC 284
 RESULT 14
 CRTL_SNNY3
 ID CRTL_SNNY3 STANDARD; PRT; 472 AA.
 AC P29273;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
 GN PDS OR CRTD OR SLR1254.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92256820; PubMed=1581575;
 RA Martinez-Ferez I.M., Vioque A.;
 RT "Nucleotide sequence of the phytoene desaturase gene from
 Synechocystis sp. PCC 6803 and characterization of a new mutation
 which confers resistance to the herbicide norflurazon.";
 RL Plant Mol. Biol. 18:981-983(1992).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RA Vioque A.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugiyama M., Sugiyama S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
 CC INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
 CC DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
 CC -!- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
 CC -!- ENZYME REGULATION: INHIBITED BY THE HERBICIDE NORFLURAZON IN A
 CC NON-COMPETITIVE WAY.
 CC -!- PATHWAY: Carotenoid biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (Probable).
 CC -!- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X62574; CAA44452.1; -;
 DR EMBL: D90909; BAA17847.1; -;
 DR PIR: S20939; S20939
 DR InterPro: IPR002937; Amino_oxidase.
 DR Pfam: PF01593; Amino_oxidase; 1.
 DR Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
 KW Membrane; Herbicide resistance; Complete proteome.
 FT NP_BIND 7 23 FAD (ADP PART) (POTENTIAL).
 FT VARIANT 195 195 R -> C (CONFERS RESISTANCE TO THE
 FT HERBICIDE NORFLURAZON).
 FT SEQUENCE 472 AA; 52920 MW; 81D089A6DAA28758 CRC64;
 Query Match 27.9%; Score 51; DB 1; Length 472;
 Best Local Similarity 45.8%; Pred. No. 36;
 Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 OY 10 LKTQVEKLRVNAKEMQALQTV 33
 DB 278 LKTMVPAPMREYEPFKQTGLEGV 301
 RESULT 15
 IMBL_RAT
 ID IMBL_RAT STANDARD; PRT; 875 AA.
 AC P52296;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear factor
 DE p97).
 DE NCBI_TaxID=10116;
 GN KPNB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Buffalo; TISSUE=Liver;
 RX MEDLINE=95183547; PubMed=7878057;
 RA Radu A., Blobel G., Moore M.M.;
 RA "Identification of a protein complex that is required for nuclear
 RT protein import and mediates docking of import substrate to distinct
 RT nucleoporins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1769-1773(1995).
 RN [2]
 RP SUBCELLULAR LOCATION, AND BINDING TO NUCLEOPORINS.
 RX MEDLINE=95327681; PubMed=7604027;
 RA Moroiu J., Hijikata M., Blobel G., Radu A.;

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Query Match      27.9%; Score 51; DB 1; Length 875;
Best Local Similarity 35.1%; Pred. No. 71;
Matches 13; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

1 RRVKEKDGDKLTQVEKLWR--EYNALKEMO--ALQTV 33
      | | | | | | | | | | | | | | | |
62 RLITSKDDPKIKAYQOORWLAIADANARREKNNYVLOTI 98

```

Search completed: April 15, 2003, 11:48:34
Job time : 8.5 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:44:50 ; Search time 22.5 seconds
(without alignments)
329.675 Million cell updates/sec

Title: US-09-445-576A-38

Perfect score: 183

Sequence: 1 RRVKEDGDLKTQVKRLWREYNALKEMQALQTVCLR 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_Organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	183	100.0	197	6 Q28008	Q28008 bos taurus
2	166	90.7	196	11 Q98PW4	Q98PW4 mus musculus
3	85.5	46.7	201	13 Q9DD44	Q9DD44 gallus gall
4	65	35.5	630	3 O13870	O13870 schizosacch
5	62	33.9	584	11 Q9CR92	Q9CR92 mus musculus
6	61	33.3	1008	16 Q9X082	Q9X082 thermotoga
7	61	33.3	7659	5 Q9N4M4	Q9N4M4 caenorhabdi
8	59	32.2	251	16 Q8UED7	Q8UED7 agrobacteri
9	58.5	32.0	428	11 Q9CWR2	Q9CWR2 mus musculus
10	58	31.7	230	4 Q9BS48	Q9BS48 homo sapien
11	58	31.7	513	11 Q9R120	Q9R120 rattus norv
12	58	31.7	517	11 Q8VEJ0	Q8VEJ0 mus musculus
13	58	31.7	535	11 Q9Z2L8	Q9Z2L8 mus musculus
14	58	31.7	631	16 Q98QP5	Q98QP5 mycoplasma
15	57.5	31.4	171	4 Q96QW4	Q96QW4 homo sapien
16	57.5	31.4	239	4 Q96A15	Q96A15 homo sapien

17	57.5	31.4	369	4 Q9H7B4	Q9H7B4 homo sapien
18	57	31.1	474	4 Q96M63	Q96M63 homo sapien
19	57	31.1	807	4 Q9H8A7	Q9H8A7 homo sapien
20	57	31.1	1191	11 P97690	P97690 rattus norv
21	57	31.1	1217	4 O60464	O60464 homo sapien
22	57	31.1	1217	11 Q9QUS3	Q9QUS3 mus musculus
23	57	31.1	1218	6 Q97594	Q97594 bos taurus
24	57	31.1	1532	4 Q9P2K1	Q9P2K1 homo sapien
25	56	30.6	73	17 Q27806	Q27806 methanobact
26	56	30.6	142	3 Q92425	Q92425 ganoderma l
27	55.5	30.3	1265	10 Q9MIT3	Q9MIT3 arabidopsis
28	55	30.1	142	3 Q92424	Q92424 ganoderma l
29	55	30.1	156	16 Q9KEA0	Q9KEA0 bacillus ha
30	55	30.1	306	17 Q27097	Q27097 methanobact
31	55	30.1	391	16 Q8ZAY8	Q8ZAY8 versinia pe
32	55	30.1	2434	8 Q9MTH5	Q9MTH5 oenothera h
33	54.5	29.8	255	3 Q9P4V6	Q9P4V6 candida boi
34	54.5	29.8	394	3 Q9HEB1	Q9HEB1 neurospora
35	54.5	29.8	659	5 Q18406	Q18406 caenorhabdi
36	54.5	29.8	759	16 Q25761	Q25761 helicobacte
37	54	29.5	319	10 Q23077	Q23077 arabidopsis
38	54	29.5	531	4 Q96EK2	Q96EK2 homo sapien
39	54	29.5	862	10 Q04649	Q04649 arabidopsis
40	54	29.5	976	10 Q9SK70	Q9SK70 arabidopsis
41	54	29.5	1011	3 Q93882	Q93882 neurospora
42	53.5	29.2	142	3 Q92420	Q92420 ganoderma f
43	53.5	29.2	455	5 Q9GYA4	Q9GYA4 leishmania
44	53.5	29.2	639	10 Q9LNA4	Q9LNA4 arabidopsis
45	53.5	29.2	952	3 Q9UTR7	Q9UTR7 schizosacch

ALIGNMENTS

RESULT 1

ID Q28008 PRELIMINARY; PRT; 197 AA.
AC Q28008;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-type lectin homolog precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARTILAGE;
RA Neame P.J., Boynton R.E.;
RT "C-type lectin homolog from bovine cartilage.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22298; AAC18614.1; -
DR HSSP; P05452; ITN3.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1..24 POTENTIAL.
FT CHAIN 25..197 C-TYPE LECTIN HOMOLOG.
SQ SEQUENCE 197 AA; 22215 MW; AACAC4280F41AC0F4 CRC64;

Query Match 100.0%; Score 183; DB 6; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRVKEDGDLKTQVKRLWREYNALKEMQALQTVCLR 36

Db 35 RRVKEDGDLKTQVKRLWREYNALKEMQALQTVCLR 70

<hr/>					
RESULT 2					
Q9EPW4	PRELIMINARY; PRT; 196 AA.				
ID Q9EPW4;					
AC Q9EPW4;					
DT 01-MAR-2001 (TREMBlrel. 16, Created)					
DT 01-NAR-2001 (TREMBlrel. 16, Last sequence update)					
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)					
DE C-type lectin superfamily 1.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=ES129/SV;					
RA Neame P.J., Grimm D.R.;					
RT "Mouse homolog of human LECSEF1, a cartilage derived C-type lectin.";					
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AF317204; AAG48620.1; -					
DR HSSP; P05452; 1HTN					
DR InterPro; IPR001304; Lectin_C.					
DR Pfam; PF00059; lectin_c; 1.					
DR SMART; SM00034; CLECT; 1.					
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.					
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.					
KW Lectin.					
SQ SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;					
<hr/>					
Query Match	90.7%; Score 166; DB 11; Length 196;				
Best Local Similarity	91.7%; Pred. No. 1e-13;				
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
Oy 1 RRVRKKGDLKTQVEKLWRVNALEKMQALQTVCCLR 36					
Db 35 RRVAKDDDLKSQVEKLWRVNALEKMQALQTVCCLR 70					
<hr/>					
RESULT 3					
Q9DDD4	PRELIMINARY; PRT; 201 AA.				
ID Q9DDD4;					
AC Q9DDD4;					
DT 01-MAR-2001 (TREMBlrel. 16, Created)					
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)					
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)					
DE Tetranectin.					
OS Gallus gallus (Chicken).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;					
OC Gallus.					
OX NCBI_TaxID=9031;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Wewer U.M.;					
RT "tetranectin in chicken.";					
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AJ277116; CAC20217.1; -					
DR HSSP; P05452; ITN3.					
DR InterPro; IPR001304; Lectin_C.					
DR Pfam; PF00059; lectin_c; 1.					
DR SMART; SM00034; CLECT; 1.					
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.					
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.					
SQ SEQUENCE 201 AA; 22172 MW; 7CF2F35D24426AE8 CRC64;					
<hr/>					
Query Match	46.7%; Score 85.5; DB 13; Length 201;				
Best Local Similarity	48.7%; Pred. No. 0.0027;				
Matches 19; Conservative 6; Mismatches 7; Indels 7; Gaps 1;					
OY 5 EKDG-----DLKTQVEKLWRVNALEKMQALQTVCCLR 36					
: : : : : :					
Db 34 KDGVLKKMIEDLKAMIDNISQEVALLKQKALQTVCCLR 72					

RC STRAIN=BRISTOL N2;
RA MEDLINE=99069613; PubMed=9851916;
RX None;
RY "Genome sequencing of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX Gattung S., Goela D., Broy M.;
RY "The sequence of C. elegans cosmid ZK973.";
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA STRAIN=BRISTOL N2;
RX Waterston R.;
RY "Direct Submission.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RD EMBL; AC006834; AAF40010.2; -
RE InterPro: IPR003103; BAG.
RF InterPro: IPR001092; HLH_basic.
RG SMART; SM00264; BAG; 1.
RH PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_2.
RW Hypothetical protein.
SX SEQUENCE 7659 AA; BBA95964D79B4FF1 CRC64;

Query Match 33.3%; Score 61; DB 5; Length 7659;
Best Local Similarity 45.7%; Pred. No. 1.7e+02;
Matches 16; Conservative 7; Mismatches 8; Indels 4; Gaps

QY 3 VKEGDKLTQVEKLWREV---NALKEMALQTV 33
| | | | : | : | : | | | | : | : | | | : |
Db 917 VGEGLNKLKSAVEEYEEVLASTNPVKEDQLQHI 951

RESULT 8
Q8UED7 PRELIMINARY; PRT; 251 AA.

AC Q8UED7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ABC transporter, nucleotide binding/ATPase protein.
GN SUFC OR ATU1823 OR AGR.C.3346.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Woo L.,
RU Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RV Chen Y.Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RW Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RX Kutayav T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RY Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
SZ Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
TA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
TB Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
TC Nestor E.W.;
TD "The genome of the natural genetic engineer Agrobacterium tumefaciens
TE C58.";
TF Science 294:2317-2323(2001).
TN [2]
RC SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RU Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RV Houmlet K., Gordon J., Vaubin M., Lartchouk O., Epp A., Liu F.,
RW Weiland C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
RX Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RY Glacio C., Slater S.;

Search completed: April 15, 2003, 11:50:14
Job time : 25.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:43:14 ; Search time 28.75 Seconds
(without alignments)
166.853 Million cell updates/sec

Title: US-09-445-576A-39

Perfect score: 185

Sequence: 1 SKSGKGKDDLRNEIDKLWRENSLREKMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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- 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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- 16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113.5	61.4	197	21	protein encoded by
2	113.5	61.4	197	21	Human breast tumou
3	113.5	61.4	206	21	Membrane-bound pro
4	113.5	61.4	206	22	Human PRO polypept
5	113.5	61.4	206	22	Human PRO1345 (UNQ
6	113.5	61.4	206	23	Human tumour-associ
7	84	45.4	180	20	H6FXTN23 fusion pr
8	84	45.4	181	20	Human tetranectin
9	84	45.4	197	20	H6FXTN123 fusion p
10	84	45.4	202	15	Human tetranectin.

11	84	45.4	202	22	AAW24034	Human EST encoded
12	84	45.4	228	20	AAW94261	CIH6FXTN123 fusio
13	79	42.7	182	7	AAW60098	Sequence of chain
14	74	40.0	52	20	AAW94254	Tetranectin polype
15	74	40.0	73	20	AAW94270	H6FXTripa fusion p
16	66	35.7	49	20	AAW94255	Tetranectin polype
17	66	35.7	65	20	AAW94263	H6FXTN12 fusion pr
18	62	33.5	69	20	AAW94271	H6FXTripb fusion p
19	62	33.5	145	20	AAW94266	H6FXTripB-UB fusio
20	62	33.5	330	20	AAW94267	H6FXScFv(CEA6)trip
21	62	33.5	331	20	AAW94268	H6FXTripBScFv(CEA6
22	62	33.5	592	20	AAW94269	H6FXScFv(CEA6)trip
23	57	30.8	382	21	AAW58776	Breast and ovarian
24	57	30.8	529	12	AAW13503	HSF. Homo sapiens
25	57	30.8	529	13	AAW24948	Sequence encoded b
26	57	30.8	529	19	AAW49093	Human wild-type he
27	57	30.8	529	21	AAW55845	Human heat shock t
28	57	30.8	783	21	AAW22939	GFP-HSF1 fusion pr
29	57	30.8	912	20	AAW94029	BsII methylase. B
30	57	30.8	1242	21	AAW53371	Human colon cancer
31	56	30.3	286	22	AAW96752	Putative p. abysssi
32	56	30.3	917	22	ABW64837	Drosophila melanog
33	55.5	30.0	386	21	AAW59268	Human huntingtin-i
34	55.5	30.0	388	18	AAW18029	Huntingtin interac
35	55.5	30.0	629	23	AAW69424	Lung small cell ca
36	55.5	30.0	676	22	AAW39666	Human polypeptide
37	55.5	30.0	699	22	AAW41452	Human polypeptide
38	55.5	30.0	914	18	AAW18030	Huntingtin interac
39	55.5	30.0	914	21	AAW59269	Human huntingtin-i
40	55.5	30.0	1090	21	AAW59270	Human huntingtin-i
41	55	29.7	84	19	AAW43027	Artificial recogni
42	55	29.7	179	18	AAW28079	Amino acid sequenc
43	55	29.7	401	22	ABW62489	Drosophila melanog
44	54.5	29.5	164	22	AAW93529	Human protein sequ
45	54	29.2	346	22	ABG21976	Novel human diagno

ALIGNMENTS

RESULT 1
AAB28526
ID AAB28526 standard; Protein; 197 AA.
XX
AC AAB28526;
XX
DT 07-FEB-2001 (first entry)
XX
DE Protein encoded by human breast tumour cDNA clone B5325.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
KW breast cancer; vaccine.
XX
OS Homo sapiens.
XX
PN WO200061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-028950.
PR 02-JUL-1999; 99US-0346327.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI: 2000-638568/61.
DR N-PSDB; AAC79471.
XX
PT A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast

dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
Homo sapiens.

WO200168848-A2.

20-SEP-2001.

28-FEB-2001; 2001WO-US06520.

01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
03-MAR-2000; 2000WO-US18702P.
06-MAR-2000; 2000US-186968P.
14-MAR-2000; 2000US-189320P.
14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000US-06688A.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191314P.
28-MAR-2000; 2000US-192655P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193053P.
30-MAR-2000; 2000WO-US08439.
04-APR-2000; 2000US-194449P.
11-APR-2000; 2000US-194647P.
11-APR-2000; 2000US-195975P.
11-APR-2000; 2000US-196000P.
11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-198820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198585P.
25-APR-2000; 2000US-199397P.
25-APR-2000; 2000US-199550P.
25-APR-2000; 2000US-199654P.
03-MAY-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.

N-PSDB; AAS46062.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumours, such as prostate and breast tumours, in mammals and
to screen for modulators of the compounds -

Claim 11; Fig 276; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats

CC and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, rectal, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders.

XX Sequence 206 AA;

Query Match 61.4%; Score 113.5; DB 22; Length 206;
Best Local Similarity 66.7%; Pred. No. 1.7e-07;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

OY 5 KGKD-DLRNEIDKLWREVNLSKEMQALQTVCLK 36
Db 47 RDKDGLKLTQIEKLWTEVNALKEIQALQTVCLR 79

RESULT 5

AAB65279

ID AAB65279 standard; Protein; 206 AA.

XX AAB65279;

XX 02-APR-2001 (first entry)

DE Human PRO1345 (UNQ700) protein sequence SEQ ID NO:403.

XX Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 08-OCT-1999; 99US-0158663.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;

FT Disulfide-bond 77..176
 FT Disulfide-bond 152..168
 FT Misc-difference 37
 FT /label= M,V

PN EP206400-A.

XX 30-DEC-1986.

XX 10-JUN-1986; 86EP-0201005.

XX 11-JUN-1985; 85NL-0001682.

XX (NEDE) NEDERLAND ORG TNO.

XX Duhl Clemmensen I, Kluff C;

XX WPI; 1986-340760/52.

XX New Tetranectin protein - purified from human blood plasma by

PT e.g. affinity chromatography on a column with coupled kringle 4

PT of plasminogen.

XX Claim 9; Page 1a; 12pp; English.

XX Tetranectin is comprised of four polypeptide chains having the
 CC formula shown in AAP60098. Tetranectin stimulates and controls the
 CC plasminogen activation resulting in a higher rate of clot lysis or
 CC fibrinolysis, esp. in the presence of blood platelets and in the
 CC presence of a complex fibrin clot from blood. It stimulates and
 CC controls the plasminogen activation in the absence of fibrin but in
 CC the presence of a cofactor such as polylysine.

XX Sequence 182 AA;

Query Match 42.7%; Score 79; DB 7; Length 182;

Best Local Similarity 55.2%; Pred. No. 0.0076;

Matches 16; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 8 DDLRNEIDKLWREVNLSKEMOALQTVCLK 36

DB 24 EELKSLRDLTLAQEVALLEKQOALQTVCLK 52

RESULT 14

AAW94254

ID AAW94254 standard; Protein; 52 AA.

XX AC AAW94254;

XX DT 26-APR-1999 (first entry)

XX Tetranectin polypeptide fragment (residues 1-52).

XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.

XX Homo sapiens.

XX WO9856906-A1.

XX 17-DEC-1998.

XX 11-JUN-1998; 98NO-DK00245.

XX 11-JUN-1997; 97DK-0000685.

XX (ETZE/) ETZERODT M.

XX (GRAV/) GRAVERSEN N J H.

XX (HOLT/) HOLTET T L.

XX (KAST/) KASTRUP J S.

XX

PI Etzerodt M, Graversen NUH, Holtet TL, Kastrup JS;

PI Larsen IK, Nielsen BB, Thogersen HC;

XX WPI; 1999-080897/07.

XX New monomer polypeptide constructs for diagnosis and therapy -

PT comprise a tetranectin trimerising structural element covalently

PT linked to at least one heterologous moiety for providing functional

PT activity

XX

PS Example 1; Page 59; 110pp; English.

XX The invention relates to the design of trimeric polypeptides using

XX polypeptide structural elements derived from the tetranectin protein

XX family. The trimeric polypeptides constructed as a monomer polypeptide

XX construct comprise at least one tetranectin trimerising structural

XX element (TTSE) which is covalently linked to at least one heterologous

XX moiety, the TTSE being capable of forming a stable complex with 2 other

XX TTSEs, with the proviso that the heterologous moiety is different from

XX any of the fusion proteins CIIH6FTN123, H6FTN123, H6FTN12, H6FTN23

XX (AAW94261 to AAW94264). The TTSE can be used for the construction of

XX conjugates with heterologous moieties such as a ligand binding

XX structure, a toxin, a detectable label, an in situ activatable substance,

XX an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,

XX a photo cross-linking agent, or a group facilitating conjugation of the

XX monomer polypeptide construct to a target. They can be used as vehicles

XX for assembling antibody fragments into oligomeric or multivalent

XX entities for generating chimeric artificial antibodies having

XX preselected pharmacokinetic and/or pharmacodynamic properties. The

XX constructs can be used for targeted gene therapy involving selective

XX delivery of the material for transfection or infection of the specific

XX population of cells. They can also be used for delivering a substance to

XX a cell or tissue or for delivering an imaging or toxin-conjugated

XX antibody to a tumour. They can also be used for prevention or treating a

XX disease or for diagnosis. The TTSE provides a stable structure which can

XX act as a vehicle for a wide variety of conjugates. The present sequence

XX represents a human tetranectin polypeptide fragment. The encoding nucleic

XX acid sequence was amplified by PCR from the plasmid clone pT7H6FTN123.

XX This is used in the construction of E. coli expression vectors for the

XX production of trimerised chimeric fusion proteins.

XX Sequence 52 AA;

Query Match 40.0%; Score 74; DB 20; Length 52;

Best Local Similarity 55.2%; Pred. No. 0.0082;

Matches 16; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 8 DDLRNEIDKLWREVNLSKEMOALQTVCLK 36

DB 24 EELKSLRDLTLAQEVALLEKQOALQTVCLK 52

RESULT 15

AAW94270

ID AAW94270 standard; protein; 73 AA.

XX AC AAW94270;

XX DT 26-APR-1999 (first entry)

XX H6FTXtripa fusion protein sequence.

XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;

XX fusion protein; ligand binding structure; toxin; enzyme; cytokine;

XX artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;

XX transfection; imaging; tumour; human; tetranectin.

XX Synthetic.

OS Homo sapiens.

XX WO9856906-A1.

PN

XX

PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-DK00245.
 XX
 PR 11-JUN-1997; 97DK-0000685.
 XX
 PA (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 DR WPI; 1999-080897/07.
 XX
 PT New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Disclosure: Fig 4; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6Fxtripa fusion protein sequence encoded by the plasmid
 CC pH6Fxtripa.
 XX
 SQ Sequence 73 AA:

Query Match 40.08; Score 74; DB 20; Length 73;
 Best Local Similarity 55.2%; Pred. No. 0.012;
 Matches 16; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 8 DDLRNEIDKLMREYNLSKMQALQTVCLK 36
 : : : : : | | | | | | | | | |
 Db 43 EELASRLDTLAQVEALLKEQQAQLOTVSLK 71

Search completed: April 15, 2003, 11:48:00
 Job time : 29.75 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:59 ; Search time 10 Seconds
(without alignments)
105.923 Million cell u

Title: US-09-445-576A-39

Perfect score:

Sequence: 1 SKSGKGKDDLRNEIDKLWREVNLSKEMQALQTVCLK 36

Scoring table: BLOSUM62

scoring table. BLOSUM02
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs. 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

rose processing. Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued patents AA:★

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCtUS_COMB1.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	113.5	61.4		197	4	US-09-602-877A-99	Sequence 99, Appl
2	84	45.4		202	1	US-08-463-486-36	Sequence 56, Appl
3	84	45.4		202	2	US-08-463-658-56	Sequence 56, Appl
4	57	30.8		529	1	US-08-178-477B-32	Sequence 32, Appl
5	57	30.8		529	4	US-09-304-121-2	Sequence 2, Appl
6	57	30.8		783	4	US-09-513-783A-176	Sequence 176, App
7	57	30.8		912	2	US-08-951-871-2	Sequence 2, Appl
8	55.5	30.0		386	4	US-09-085-199B-2	Sequence 2, Appl
9	55.5	30.0		914	4	US-09-085-199B-4	Sequence 4, Appl
10	55.5	30.0		1090	4	US-09-085-199B-5	Sequence 5, Appl
11	55	29.7		84	1	US-08-452-592B-9	Sequence 9, Appl
12	53	28.6		84	1	US-08-452-592B-8	Sequence 8, Appl
13	53	28.6		2710	2	US-08-568-459A-12	Sequence 12, Appl
14	53	28.6		2710	2	US-08-487-826B-12	Sequence 12, Appl
15	53	28.6		2710	4	US-09-210-288-12	Sequence 12, Appl
16	53	28.6		3060	2	US-08-487-826B-14	Sequence 14, Appl
17	52	28.1		77	1	US-08-178-477B-29	Sequence 29, Appl
18	52	28.1		236	4	US-09-134-001C-3704	Sequence 3704, Ap
19	52	28.1		257	2	US-08-715-204-6	Sequence 6, Appl
20	52	28.1		257	3	US-09-162-597-6	Sequence 6, Appl
21	52	28.1		691	1	US-08-178-477B-2	Sequence 2, Appl
22	51.5	27.8		454	4	US-09-470-512A-8	Sequence 8, Appl
23	50	27.0		42	3	US-08-956-307B-1	Sequence 1, Appl
24	50	27.0		76	3	US-08-958-307B-17	Sequence 17, Appl
25	50	27.0		84	1	US-08-452-592B-6	Sequence 6, Appl
26	50	27.0		84	1	US-08-452-592B-10	Sequence 10, Appl
27	50	27.0		546	2	US-09-067-351-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

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US-06-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND
; TITLE OF INVENTION: AND DIAGNOSIS OF
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows version
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
; US-06-602-877A-99

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Query Match 61.4%; Score 113.5; DB 4; Length.197;
Best Local Similarity 66.7%; Pred. No. 4.5e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1

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QY      5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36  
          : ||||| :||||| :||||| :||||| :||||| :  
Db     38 RDKGDLKTOIEKLWTEVNALKEIOALOTVCLR 70
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RESULT 2

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RE5011 2
US-08-469-486-56
Sequence 56, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thøgersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Eizerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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Query Match 30.8%; Score 57; DB 1; Length 529;
Best Local Similarity 37.1%; Pred. No. 6.5;
Matches 13; Conservative 7; Mismatches 7; Indels


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NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: New England Biolabs, Inc.
STREET: 32 Tozer Road
CITY: Beverly
STATE: MA
COUNTRY: US
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951.871
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 978-927-5054
TELEFAX: 978-927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-951-871-2

Query Match 30.8%; Score 57; DB 2; Length 912;
Best Local Similarity 37.9%; Pred. No. 12;
Matches 11; Conservative 5; Mismatches 13; Indels 0;

QY 7 KDLRNEIDKLWREVNSLKEMOALQTVCL 35
| : ||| ||| | : | : |
Db 130 KEXIKNEFKLWNEANEVNEYGKLKDYLL 158

RESULT 8
US-09-085-1998-2
Sequence 2, Application US/090851998
Patent No. 6235879
GENERAL INFORMATION:
APPLICANT: Hayden. Michael R.
APPLICANT: Hackam, Abigail
APPLICANT: Huq, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
TITLE OF INVENTION: Huntington's Disease Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: Huntington-interacting protein
;
US-09-085-199B-2
;
Query Match 30.0%; Score 55.5; DB 4; Length 386;
Best Local Similarity 33.3%; Pred. No. 7.2;
Matches 11; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
;
QY 1 SKSGKGKDDLNRNEIDKLRVNSLK-EMQALQT 32
;::: ||: : |::|:: || ::::
DB 113 SONGVNKDEKDHIERLYREISGLKAQLENMKT 145

RESULT 9
US-09-085-199B-4
; Sequence 4, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 914
; TYPE: amino acid
; TOPOLOGY: linear
;
Query Match 30.0%; Score 55.5; DB 4; Length 1090;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 11; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
;
QY 1 SKSGKGKDDLNRNEIDKLRVNSLK-EMQALQT 32
;::: ||: : |::|:: || ::::
DB 417 SONGVNKDEKDHIERLYREISGLKAQLENMKT 449

; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: Huntington-interacting protein
;
US-09-085-199B-2
;
Query Match 30.0%; Score 55.5; DB 4; Length 914;
Best Local Similarity 33.3%; Pred. No. 19;
Matches 11; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
;
QY 1 SKSGKGKDDLNRNEIDKLRVNSLK-EMQALQT 32
;::: ||: : |::|:: || ::::
DB 241 SONGVNKDEKDHIERLYREISGLKAQLENMKT 273

RESULT 10
US-09-085-199B-5
; Sequence 5, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-013US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1090
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: Huntington-interacting protein
;
US-09-085-199B-5
;
Query Match 30.0%; Score 55.5; DB 4; Length 1090;
Best Local Similarity 33.3%; Pred. No. 24;
Matches 11; Conservative 14; Mismatches 7; Indels 1; Gaps 1;
;
QY 1 SKSGKGKDDLNRNEIDKLRVNSLK-EMQALQT 32
;::: ||: : |::|:: || ::::
DB 417 SONGVNKDEKDHIERLYREISGLKAQLENMKT 449
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: ZIP: 01760-5035
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: DOS 6.22
: SOFTWARE: WordPerfect Version 6.1
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 05/08/452,592B
: FILING DATE: 25 May 1995
: CLASSIFICATION: 530
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/068,948
: FILING DATE: 25 May 1993
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Donahue, Richard J.
: NAME: Lamming, John H.
: NAME: Ranucci, Vincent J.
: REGISTRATION NUMBER: 22,062 (Donahue)
: REGISTRATION NUMBER: 34,857 (Lamming)
: REGISTRATION NUMBER: 29,579 (Ranucci)
: REFERENCE/DOCKET NUMBER: NA-1096D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 508-233-4510
: TELEFAX: 508-233-5167
:
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 84 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: US-08-452-592B-8
:
: Query Match 28.6%; Score 53; DB 1; Length 84;
: Best Local Similarity 52.4%; Pred. No. 2.8;
: Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
:
: QY 9 DLRNEIDKLWREYNSLKEMQA 29
: ||::: || ||| |||:: |
:
: Db 45 DLANKVAQLREVRSLKDKAA 65
:
: RESULT 13
: US-08-568-459A-12
: Sequence 12, Application US/08568459A
: Patent No. 5849306
: GENERAL INFORMATION:
: APPLICANT: Sim, Kim L.
: APPLICANT: Chitnis, Chetan
: APPLICANT: Miller, Louis H.
: APPLICANT: Peterson, David S.
: APPLICANT: Su, Xin-zhaun
: APPLICANT: Wellemis, Thomas E.
: TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobbe Martens Olson & Bear
: STREET: 620 Newport Center Drive 16th Floor
: CITY: Newport Beach
: STATE: California
: COUNTRY: US
: ZIP: 92660
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/568,459A
: FILING DATE: 07-DEC-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Israelsen, Ned
: REGISTRATION NUMBER: 29,655

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;; REFERENCE/DOCKET NUMBER: NIH121.001CP1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 235-8550
;; TELEFAX: (619) 235-0176
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2710 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORGANISM: Plasmodium falciparum
US-08-568-459A-12

Query Match      28.6%; Score 53; DB 2; Length 2710;
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 KSGKGKDDLRLNEIDKLRN 22
Db 547 KSGKGHDDIEEKLKFCDEKN 567

RESULT 14
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-487-826B-12

Query Match      28.6%; Score 53; DB 2; Length 2710;
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 KSGKGKDDLRLNEIDKLRN 22
Db 547 KSGKGHDDIEEKLKFCDEKN 567

RESULT 15
US-09-210-288-12
; Sequence 12, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/210,288
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fuller, Michael
; REGISTRATION NUMBER: 36,516
; REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-09-210-288-12

Query Match      28.6%; Score 53; DB 4; Length 2710;
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 KSGKGKDDLRLNEIDKLRN 22
Db 547 KSGKGHDDIEEKLKFCDEKN 567

Search completed: April 15, 2003, 11:51:52
Job time : 12 secs
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2003, 11:50:25 ; Search time 10.Seconds
(without alignments)
220.090 Million cell updates/sec

Title: US-09-445-576a-39

Perfect score: 185

Sequence: 1 SKSGKGKDDLRLNEIDKLWREVNLSKEMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	185	100.0	36	9	US-09-987-107-42		Sequence 42, Appl
2	124.5	67.3	36	9	US-09-987-107-41		Sequence 41, Appl
3	113.5	61.4	197	10	US-09-745-288-99		Sequence 99, Appl
4	113.5	61.4	206	9	US-09-938-418-10		Sequence 10, Appl
5	113.5	61.4	206	9	US-09-992-598-403		Sequence 403, Appl
6	113.5	61.4	206	9	US-09-989-293A-403		Sequence 403, Appl
7	113.5	61.4	206	9	US-09-989-735-403		Sequence 403, Appl
8	113.5	61.4	206	9	US-09-990-444-403		Sequence 403, Appl
9	113.5	61.4	206	9	US-09-989-730-403		Sequence 403, Appl
10	113.5	61.4	206	9	US-09-990-436-403		Sequence 403, Appl
11	113.5	61.4	206	9	US-09-991-181-403		Sequence 403, Appl
12	113.5	61.4	206	9	US-09-993-687-403		Sequence 403, Appl
13	113.5	61.4	206	9	US-09-989-734-403		Sequence 403, Appl
14	113.5	61.4	206	9	US-10-127-966-2		Sequence 2, Appl
15	113.5	61.4	206	9	US-09-997-653-403		Sequence 403, Appl
16	113.5	61.4	206	9	US-10-174-590-276		Sequence 276, Appl
17	113.5	61.4	206	9	US-10-176-758-276		Sequence 276, Appl
18	113.5	61.4	206	9	US-10-175-737-276		Sequence 276, Appl
19	113.5	61.4	206	9	US-09-993-667-403		Sequence 403, Appl

20	113.5	61.4	206	9	US-10-173-706-276	Sequence 276, App
21	113.5	61.4	206	9	US-10-175-738-276	Sequence 276, App
22	113.5	61.4	206	9	US-10-175-752-276	Sequence 276, App
23	113.5	61.4	206	9	US-10-176-482-276	Sequence 276, App
24	113.5	61.4	206	9	US-10-176-757-276	Sequence 276, App
25	113.5	61.4	206	9	US-10-176-913-276	Sequence 276, App
26	113.5	61.4	206	9	US-10-180-552-276	Sequence 276, App
27	113.5	61.4	206	9	US-10-180-557-276	Sequence 276, App
28	113.5	61.4	206	9	US-09-990-438-403	Sequence 403, App
29	113.5	61.4	206	9	US-09-990-562-403	Sequence 403, App
30	113.5	61.4	206	9	US-09-997-428-403	Sequence 403, App
31	113.5	61.4	206	9	US-09-997-666-403	Sequence 403, App
32	113.5	61.4	206	9	US-10-173-700-276	Sequence 276, App
33	113.5	61.4	206	9	US-10-174-572-276	Sequence 276, App
34	113.5	61.4	206	9	US-10-174-579-276	Sequence 276, App
35	113.5	61.4	206	9	US-10-174-582-276	Sequence 276, App
36	113.5	61.4	206	9	US-10-174-588-276	Sequence 276, App
37	113.5	61.4	206	9	US-10-175-739-276	Sequence 276, App
38	113.5	61.4	206	9	US-10-175-740-276	Sequence 276, App
39	113.5	61.4	206	9	US-10-175-743-276	Sequence 276, App
40	113.5	61.4	206	9	US-10-176-488-276	Sequence 276, App
41	113.5	61.4	206	9	US-10-176-492-276	Sequence 276, App
42	113.5	61.4	206	9	US-10-176-747-276	Sequence 276, App
43	113.5	61.4	206	9	US-10-176-750-276	Sequence 276, App
44	113.5	61.4	206	9	US-10-176-985-276	Sequence 276, App
45	113.5	61.4	206	9	US-10-176-987-276	Sequence 276, App

ALIGNMENTS

RESULT 1
US-09-987-107-42
; Sequence 42, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Carcharhinus springeri
; US-09-987-107-42

Query Match 100.0%; Score 185; DB 9; Length 36;
Best Local Similarity 100.0%; Pred No. 2.8e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKSGKGKDDLRLNEIDKLWREVNLSKEMQALQTVCLK 36
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DB 1 SKSGKGKDDLRLNEIDKLWREVNLSKEMQALQTVCLK 36

RESULT 2
US-09-987-107-41
; Sequence 41, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES

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; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-987-107-41

Query Match 67.3%; Score 124.5; DB 9; Length 36;
Best Local Similarity 72.7%; Pred. No. 3.5e-10;
Matches 24; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLREVNLSKEMQALQTVCLK 36
Db 4 KKDGLTKTQIEKLVNALKEMQALQTVCLR 36

RESULT 3
US-09-745-288-99
; Sequence 99, Application US/09745288
; Patent No. US20010018059A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-745-288-99

Query Match 61.4%; Score 113.5; DB 10; Length 197;
Best Local Similarity 66.7%; Pred. No. 7.7e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLREVNLSKEMQALQTVCLK 36
Db 38 RDKDGLTKTQIEKLVNALKEMQALQTVCLR 70

RESULT 4
US-09-938-418-10
; Sequence 10, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Polakis, Paul
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
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; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-938-418-10

Query Match 61.4%; Score 113.5; DB 9; Length 206;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLREVNLSKEMQALQTVCLK 36
Db 47 RDKDGLTKTQIEKLVNALKEMQALQTVCLR 79

RESULT 5
US-09-992-598-403
; Sequence 403, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
```

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 61.4%; Score 113.5; DB 9; Length 206;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGRD-DLRNEIDKLREVNLSKEMQALQTVCLK 36
DB 47 RDXDGLTKQIEKLTWTEVNAKIEQALQTVCLR 79

RESULT 7
US-09-989-735-403
; Sequence 403, Application 05/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Iivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT FILING DATE: 2001-11-19
PRIORITY APPLICATION NUMBER: US/09/989,735
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-11-12
PRIORITY APPLICATION NUMBER: 60/065186
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25 PRIOR FILING DATE: 1998-07-07
26 PRIOR APPLICATION NUMBER: 60/091982
27 PRIOR FILING DATE: 1998-07-07
28 PRIOR APPLICATION NUMBER: 60/092182
29 PRIOR FILING DATE: 1998-07-09

Query Match 61.4%; Score 113.5; DB 9; Length 206;

Best Local Similarity 66.7%; Pred. No. 8.1e-08;

Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KCGD-DLRNEIDKLRVNSLKEQALQTVCLK 36
DB 47 RDKDGLTKQIEKLTVEVNALEQALQTVCLR 79

RESULT 8

US-09-990-444-403
Sequence 403, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14

1 PRIOR APPLICATION NUMBER: 60/049787
2 PRIOR FILING DATE: 1997-06-16
3 PRIOR APPLICATION NUMBER: 60/062250
4 PRIOR FILING DATE: 1997-10-17
5 PRIOR APPLICATION NUMBER: 60/065186
6 PRIOR FILING DATE: 1997-11-12
7 PRIOR APPLICATION NUMBER: 60/065311
8 PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 61.4%; Score 113.5; DB 9; Length 206;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEQALQTVCLK 36
Db 47 RKDGDGDKTQIEKLWTEVNALKEIQALQTVCLR 79

RESULT 9

US-09-989-730-403
; Sequence 403; Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-09

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; Publication No. US20020198148A1
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; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Baker, Kevin P.
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; APPLICANT: Bolstein, David.
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; APPLICANT: Desnoyers, Luc.
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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Fong, Sherman
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; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Gritsen, Mary E.
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kijavlin, Ivar J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Pan, James
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Roy, Margaret Ann.
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Watanabe, Colin K.
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; APPLICANT: Williams, P. Mickey
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; APPLICANT: Wood, William I.
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; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; Sequence 403, Application US/0999118
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnovers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
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; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Williams,P. Mickey
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: Secrets Encoding Tr
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/9/9
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607

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DB      47  RKDGDGLKTOIEKLWTEVNAKEIQALQOTVCCLR 79
RESULT 13
US-0989-734-403
; Sequence 403, Application US/0989734
; Publication No. US2003000331A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembra
; FILE REFERENCE: P2730PLC64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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57	PRIOR APPLICATION NUMBER: 60/091982
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59	PRIOR APPLICATION NUMBER: 60/092182
60	PRIOR FILING DATE: 1998-07-09

Query Match 61.4%; Score 113.5; DB 9; Length 206;

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Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

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RESULT 14

US-10-127-966-2

03 10 127 300 2 ; Sequence 2, Application US/10127966

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: Publication No. US20030003507A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J
: APPLICANT: Eaton, Dan L.
: APPLICANT: Goddard, Audrey
: APPLICANT: Gurney, Austin L.
: APPLICANT: Wood, William I.
: APPLICANT: Wu, Thomas D.
: TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
: TITLE OF INVENTION: Treatment of Tumor
: FILE REFERENCE: P5024R1
: CURRENT APPLICATION NUMBER: US/10/127,966
: CURRENT FILING DATE: 2002-04-23
: PRIOR APPLICATION NUMBER: US 60/097,022
: PRIOR FILING DATE: 1998-08-18
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: 1999-06-02
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: 2000-03-30
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: US 09/941,992
: PRIOR FILING DATE: 2001-08-28
: PRIOR APPLICATION NUMBER: US 09/990,711
: PRIOR FILING DATE: 2001-11-14
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 2
: LENGTH: 206
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-127-966-2

Query Match 61.4%; Score 113.5; DB 9; Length 206;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

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: Publication No. US20030008297A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730PIC38

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Search completed: April 15, 2003, 12:06:36
Job time : 10 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:05 ; Search time 183 Seconds
(without alignments)
126.833 Million cell updates/sec

Title: US-09-445-576A-39

Perfect score: 185

Sequence: 1 SKSGKGKDLRLNEIDKLWREVNLSKEMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	100.0	36	18 US-09-445-576-38	Sequence 38, Appl
2	185	100.0	36	23 US-09-987-107-42	Sequence 42, Appl
3	185	100.0	166	21 US-09-791-537-62196	Sequence 62196, A
4	124.5	67.3	36	18 US-09-445-576-37	Sequence 37, Appl
5	124.5	67.3	36	23 US-09-987-107-41	Sequence 41, Appl
6	124.5	67.3	197	21 US-09-791-537-145359	Sequence 145359,

7	113.5	61.4	197	1	PCT-US02-19669-55	Sequence 55, Appl
8	113.5	61.4	197	16	US-09-288-950-99	Sequence 99, Appl
9	113.5	61.4	197	17	US-09-346-327-99	Sequence 99, Appl
10	113.5	61.4	197	20	US-09-687-507-99	Sequence 99, Appl
11	113.5	61.4	197	20	US-09-687-507A-99	Sequence 99, Appl
12	113.5	61.4	197	21	US-09-745-288-99	Sequence 99, Appl
13	113.5	61.4	197	21	US-09-778-531-99	Sequence 99, Appl
14	113.5	61.4	197	21	US-09-791-537-25686	Sequence 25686, A
15	113.5	61.4	197	25	US-10-177-293-55	Sequence 55, Appl
16	113.5	61.4	206	1	PCT-US02-12619-2	Sequence 2, Appl
17	113.5	61.4	206	1	PCT-US02-19669-57	Sequence 57, Appl
18	113.5	61.4	206	21	US-09-709-238-403	Sequence 403, App
19	113.5	61.4	206	23	US-09-938-418-10	Sequence 10, Appl
20	113.5	61.4	206	23	US-09-941-992-403	Sequence 403, App
21	113.5	61.4	206	23	US-09-989-379-403	Sequence 403, App
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42	113.5	61.4	206	23	US-09-990-438-403	Sequence 403, App
43	113.5	61.4	206	23	US-09-990-439-403	Sequence 403, App
44	113.5	61.4	206	23	US-09-990-440-403	Sequence 403, App
45	113.5	61.4	206	23	US-09-990-441-403	Sequence 403, App

ALIGNMENTS

RESULT 1
US-09-445-576-38
; Sequence 38, Application US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Heilskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjolier
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN -1
; CURRENT APPLICATION NUMBER: US/09/445,576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: shark
US-09-445-576-38

Query Match 100.0%; Score 185; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
 |||
 Db 1 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 36

RESULT 2

US-09-987-107-42
 ; Sequence 42, Application US/09987107
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; APPLICANT: MOESTRUP, Soren
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA
 ; CURRENT APPLICATION NUMBER: US/09/987.107
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 42
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Carcharhinus springeri
 US-09-987-107-42

Query Match 100.0%; Score 185; DB 23; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.2e-17;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
 |||
 Db 1 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 36

RESULT 3

US-09-791-537-62196
 ; Sequence 62196, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 62196
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Carcharhinus springeri
 US-09-791-537-62196

Query Match 100.0%; Score 185; DB 21; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
 |||
 Db 4 SKSGKGDDLRNEIDKLWREVNSLKEMQALQTVCLK 39

RESULT 4

US-09-445-576-37
 ; Sequence 37, Application US/09445576
 ; GENERAL INFORMATION:

; APPLICANT: Thogersen, Hans Christian
 ; APPLICANT: Etzerodt, Michael
 ; APPLICANT: Holtet, Thor Las
 ; APPLICANT: Graversen, Niels Jonas Heilskov
 ; APPLICANT: Kasturup, Jette Sandholm
 ; APPLICANT: Nielsen, Bettina Bryde
 ; APPLICANT: Larsen, Ingrid Kjoller
 ; TITLE OF INVENTION: Trimerising module
 ; FILE REFERENCE: THOGERSEN -1
 ; CURRENT APPLICATION NUMBER: US/09/445,576
 ; CURRENT FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: PCT/DK98/00245
 ; PRIOR FILING DATE: 1998-06-11
 ; PRIOR APPLICATION NUMBER: DK 0685/97
 ; PRIOR FILING DATE: 1997-06-11
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 37
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: bovine
 US-09-445-576-37

Query Match 67.3%; Score 124.5; DB 18; Length 36;
 Best Local Similarity 72.7%; Pred. No. 4.7e-09;
 Matches 24; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
 |||
 Db 4 KEKGGDLKTQVEKLWREVNALKEMQALQTVCLR 36

RESULT 5

US-09-987-107-41
 ; Sequence 41, Application US/09987107
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; APPLICANT: MOESTRUP, Soren
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSENIA
 ; CURRENT APPLICATION NUMBER: US/09/987,107
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 41
 ; LENGTH: 36
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-09-987-107-41

Query Match 67.3%; Score 124.5; DB 23; Length 36;
 Best Local Similarity 72.7%; Pred. No. 4.7e-09;
 Matches 24; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
 |||
 Db 4 KEKGGDLKTQVEKLWREVNALKEMQALQTVCLR 36

RESULT 6

US-09-791-537-145359
 ; Sequence 145359, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 145359
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-791-537-145359

Query Match 67.3%; Score 124.5; DB 21; Length 197;
Best Local Similarity 72.7%; Pred. No. 3.8e-08;
Matches 24; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEMQALQTVCLK 36
: || ||| : ||| ||| ||| ||| ||| ||| ||| :
DB 38 RKDGLKTKQIEKLWTEVNALEIQAQTVCCLR 70

RESULT 7
PCT-US02-19669-55
; Sequence 55, Application PC/TUS0219669
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669-55

Query Match 61.4%; Score 113.5; DB 1; Length 197;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEMQALQTVCLK 36
: || ||| : ||| ||| ||| ||| ||| ||| :
DB 38 RKDGLKTKQIEKLWTEVNALEIQAQTVCCLR 70

RESULT 8
US-09-288-950-99
; Sequence 99, Application US/09288950
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.446C3
; CURRENT APPLICATION NUMBER: US/09/288,950
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-288-950-99

Query Match 61.4%; Score 113.5; DB 16; Length 197;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEMQALQTVCLK 36
: || ||| : ||| ||| ||| ||| ||| ||| :
DB 38 RKDGLKTKQIEKLWTEVNALEIQAQTVCCLR 70

RESULT 9
US-09-346-327-99
; Sequence 99, Application US/09346327
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.446C4
; CURRENT APPLICATION NUMBER: US/09/346,327
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-346-327-99

Query Match 61.4%; Score 113.5; DB 17; Length 197;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEMQALQTVCLK 36
: || ||| : ||| ||| ||| ||| ||| ||| :
DB 38 RKDGLKTKQIEKLWTEVNALEIQAQTVCCLR 70

RESULT 10
US-09-687-507-99
; Sequence 99, Application US/09687507
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.446C6
; CURRENT APPLICATION NUMBER: US/09/687,507
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-687-507-99

Query Match 61.4%; Score 113.5; DB 20; Length 197;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLRVNSLKEMQALQTVCLK 36
: || ||| : ||| ||| ||| ||| ||| ||| :
DB 38 RKDGLKTKQIEKLWTEVNALEIQAQTVCCLR 70

;; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
;; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
;; FILE REFERENCE: MRI-038

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	185	100.0	36	5	US-09-445-576A-39		Sequence 39, Appl
2	124.5	67.3	36	5	US-09-445-576A-38		Sequence 38, Appl
3	113.5	61.4	197	1	PCr-US02-19669A-55		Sequence 55, Appl
4	113.5	61.4	206	1	PCr-US02-19669A-57		Sequence 57, Appl
5	113.5	61.4	206	5	US-09-989-733-403		Sequence 403, App
6	113.5	61.4	206	5	US-09-992-643-403		Sequence 403, App
7	113.5	61.4	206	6	US-10-125-923A-276		Sequence 276, App
8	113.5	61.4	206	6	US-10-205-892-276		Sequence 276, App
9	113.5	61.4	206	6	US-10-174-575-276		Sequence 276, App
10	113.5	61.4	206	6	US-10-174-575A-276		Sequence 276, App
11	113.5	61.4	206	6	US-10-187-755-276		Sequence 276, App
12	113.5	61.4	206	6	US-10-187-749-276		Sequence 276, App
13	113.5	61.4	206	6	US-10-196-672-276		Sequence 276, App
14	113.5	61.4	206	6	US-10-194-486-276		Sequence 276, App
15	89	48.1	36	5	US-09-445-576A-37		Sequence 37, Appl
16	84	45.4	36	5	US-09-445-576A-36		Sequence 36, Appl
17	84	45.4	52	5	US-09-445-576A-71		Sequence 71, Appl
18	84	45.4	180	5	US-09-445-576A-27		Sequence 27, Appl
19	84	45.4	181	5	US-09-445-576A-7		Sequence 7, Appl
20	84	45.4	197	5	US-09-445-576A-25		Sequence 25, Appl
21	84	45.4	202	1	PCr-US02-38407-13		Sequence 13, Appl
22	84	45.4	202	5	US-09-992-095B-62		Sequence 62, Appl
23	84	45.4	202	5	US-09-999-570-62		Sequence 62, Appl
24	84	45.4	202	6	US-10-154-678-62		Sequence 62, Appl
25	84	45.4	202	6	US-10-276-781-1559		Sequence 1559, Ap
26	84	45.4	228	5	US-09-445-576A-24		Sequence 24, Appl

01.13, SCORE 113.5, DV 1, LENGTH 206,

APPLICANT: Baker, Kevin P.

;
; PRIOR APPLICATION NUMBER:

APPLICANT: Baker, Kevin P.

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; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-276

Query Match
Best Local Similarity 61.4%; Score 113.5; DB 6; Length 206;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLWREVNSLKEMOALQTVCLK 36
Db 47 RDKGDLTKTOIEKLWTEVNALEIQALQTVCLR 79

RESULT 14
US-10-194-486-276
; Sequence 276, Application US/10194486
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/194,486
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 276
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-486-276

Query Match
Best Local Similarity 61.4%; Score 113.5; DB 6; Length 206;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

QY 5 KGKD-DLRNEIDKLWREVNSLKEMOALQTVCLK 36
Db 47 RDKGDLTKTOIEKLWTEVNALEIQALQTVCLR 79

RESULT 15
US-09-445-576A-37
; Sequence 37, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Murine
US-09-445-576A-37

Query Match
Best Local Similarity 48.1%; Score 89; DB 5; Length 36;
Matches 20; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 3 SKGKGDDLNEIDKLWREVNSLKEMOALQTVCLK 36
Db 3 SSKMFEELKNRMDVLAQEVALLEKQALQTVCLK 36

Search completed: April 15, 2003, 12:05:49
Job time : 24.25 secs
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:44 ; Search time 11.75 Seconds
(without alignments)
294.540 Million cell updates/sec

Title: US-09-445-576A-39

Perfect score: 185

Sequence: 1 SKSGKGKDDLREIDKLRVNSLKEMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	100.0	166	1 A37289	tetranectin homolo
2	89	48.1	202	2 JC4031	tetranectin precu
3	84	45.4	202	1 TTHUN	tetranectin precu
4	61	33.0	1040	2 D81379	transmembrane efl
5	60.5	32.7	489	2 S05474	keratin 8, type II
6	59	31.9	582	2 B70389	translation elonga
7	57	30.8	448	2 S52751	heat shock transcr
8	57	30.8	503	2 A40583	heat shock transcr
9	57	30.8	529	2 A41137	heat shock transcr
10	56	30.3	281	2 F75216	hypothetical prote
11	56	30.3	547	2 A56575	puff-specific nucl
12	56	30.3	1010	2 B37227	Na+/K+-exchanging
13	55.5	30.0	601	2 S33377	p63 protein - huma
14	55	29.7	451	2 JC4199	heat-shock protein
15	55	29.7	635	2 F90072	conserved hypothet
16	55	29.7	654	2 T32623	hypothetical prote
17	54.5	29.5	164	2 JC7112	MaF protein homol
18	54	29.2	123	2 S34019	hypothetical prote
19	54	29.2	232	2 B90230	hypothetical prote
20	54	29.2	690	2 T27508	hypothetical prote
21	53.5	28.9	614	2 T19539	hypothetical prote
22	53.5	28.9	627	2 T19542	hypothetical prote
23	53.5	28.9	1844	2 T51890	related to Nup98-N
24	53	28.6	102	2 S57536	hypothetical prote
25	53	28.6	555	2 H89957	formyltetrahydrof
26	53	28.6	559	2 T43071	activation/secreti
27	53	28.6	589	2 T59340	transcription fact
28	53	28.6	1013	1 S00801	Na+/K+-exchanging
29	53	28.6	3078	2 T28432	variant-specific s

30	52.5	28.4	241	2 S73170	ribosomal protein
31	52	28.1	138	2 B69465	transcription regu
32	52	28.1	156	2 D83769	hypothetical prote
33	52	28.1	229	2 S78375	ribosomal protein
34	52	28.1	257	2 E89632	protein Fl3E6.1 li
35	52	28.1	285	2 G72415	sensor histidine k
36	52	28.1	691	1 A36295	heat shock transcr
37	52	28.1	1597	2 S68420	citron - mouse
38	52	28.1	1679	2 S48385	hypothetical prote
39	52	28.1	2677	2 A38194	desmoplakin I - hu
40	51.5	27.8	454	2 S65970	replicative DNA he
41	51.5	27.8	633	2 T41332	casp homolog - fis
42	51.5	27.8	889	2 H96006	hypothetical prote
43	51.5	27.8	927	2 AG1739	transmembrane prot
44	51.5	27.8	945	2 S48369	26S proteasome reg
45	51	27.6	328	1 S10200	carbonate dehydrat

ALIGNMENTS

RESULT 1

A37289 tetranectin homolog - reef shark
C:Species: Carcharhinus springeri (reef shark)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A37289; A37287
R:Neame, P.J.; Young, C.N.; Treep, J.T.
Protein Sci. 1, 161-168, 1992
A:Title: Primary structure of a protein isolated from reef shark Carcharhinus springeri
A:Reference number: A37289; MUID:93284081; PMID:1304877
A:Accession: A37289
A:Molecule type: protein
A:Residues: 1-166 <NE2>
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: cartilage
F:37-160/Domain: C-type lectin homology <LCH>
F:37-47,64-160,136-152/Disulfide bonds: #status predicted

Query Match 100.0%; Score 185; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKSGKGKDDLREIDKLRVNSLKEMQALQTVCLK 36
|||||

Db 4 SKSGKGKDDLREIDKLRVNSLKEMQALQTVCLK 39
|||||

RESULT 2

JC4031 tetranectin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C:Accession: JC4031
R:Sorensen, C.B.; Berglund, L.; Petersen, T.E.
Gene 152, 243-245, 1995
A:Title: Cloning of a cDNA encoding murine tetranectin.
A:Reference number: JC4031; MUID:95137396; PMID:7835708
A:Accession: JC4031
A:Molecule type: mRNA
A:Residues: 1-202 <SOR>
A:Cross-references: EMBL:X79199; NID:g671561; PIDN:CAA55791.1; PID:g671562
A:Experimental source: lung
C:Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C:Superfamily: tetranectin; C-type lectin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-202/Product: tetranectin #status predicted <MAT>
F:71-197/Domain: C-type lectin homology <LCH>

Query Match 48.1%; Score 89; DB 2; Length 202;
Best Local Similarity 58.8%; Pred. No. 0.00082;
Matches 20; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Db 148 KGKQECMDSKLLAMKHENEALWREVASLRQKHAQQ 182

||||| : ||||| ||:: | |

RESULT 9
A41137
heat shock transcription factor 1 - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-2000
C:Accession: A41137
R:Rabindran, S.K.; Giorgi, G.; Clos, J.; Wu, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 6906-6910, 1991
A>Title: Molecular cloning and expression of a human heat shock factor, HSF1.
A:Reference number: A41137; MUID:91334376; PMID:18711105
A:Accession: A41137
A:Molecule type: mRNA
A:Residues: 1-529 <PAB>
A:CROSS-references: GB:M64673; NID:g184402; PIDN:AAA52695.1; PID:g1844403
C:Genetics:
A:Gene: GDB:HSF1
A:CROSS-references: GDB:128783; OMIM:140580
A:Map position: 8q24.3-8q24.3
C:Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding domain ho
C:Keywords: DNA binding; leucine zipper; transcription regulation
F:1824/Domain: HSF DNA-binding domain homology <HSE>

Query Match 30.8%; Score 57; DB 2; Length 529;
Best Local Similarity 37.1%; Pred. No. 23;
Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

Qy 5 KGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
||| : ||| ||:: | |

Db 148 KGKQECMDSKLLAMKHENEALWREVASLRQKHAQQ 182

RESULT 10
F75216
hypothetical protein PAB2181 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F75216
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A:Reference number: A75001
A:Accession: F75216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <KAW>
A:CROSS-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49181.1; PID:g545
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2181

Query Match 30.3%; Score 56; DB 2; Length 281;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 5 KGKDDLNRNEIDKLWREVNSLKE'26
| : : | : : | | | | |

Db 246 KKKELENKVKELEEVNKLE 267

RESULT 11
A56575
puff-specific nuclear protein Bx42 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000
C:Accession: A56575
R:Wieland, C.; Mann, S.; von Besser, H.; Saunweber, H.
Chromosoma 101, 517-525, 1992
A>Title: The Drosophila nuclear protein Bx42, which is found in many puffs on polyten
A:Reference number: A56575; MUID:93048378; PMID:1424996

```

A:Accession: A56575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <WIE>
A:Cross-references: GB:X64536; GB:S48763; NID:98391; PIDN:CAA45834.1; PID:98392
A:Note: sequence extracted from NCBI backbone (NCBIN:118716, NCBIPI:118718)
C:Genetics:
A:Gene: FlyBase:Bx42
A:Cross-references: FlyBase:FBgn0004856
C:Superfamily: Caenorhabditis elegans hypothetical protein T27F2.1

Query Match 30.3%; Score 56; DB 2; Length 547;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 KSGKGDLLRNEIDKLWREVNSL 24
DB 431 SGYGDDAEYNVYDKWRDSENTL 452

RESULT 12
B37227
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Apr-2002
C:Accession: B37227; I50395
R:Takeyasu, K.; Lemas, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 1990
A:Title: Stability of Na(+)-K(+) ATPase alpha-subunit isoforms in evolution.
A:Reference number: A37227; MUID:91023019; PMID:2171348
A:Accession: B37227
A:Molecule type: mRNA
A:Residues: 1-1010 <TA2>
A:Cross-references: GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212408
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
F:574-770/Domain: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr
F:202,470/Binding site: carboxylate-binding domain homology <ATN>
F:363/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:495/Binding site: ATP (Lys) #status predicted

Query Match 30.3%; Score 56; DB 2; Length 1010;
Best Local Similarity 40.0%; Pred. No. 62;
Matches 14; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

QY 2 KSGKGDLLRNEIDKLWREVNSLKEMQALQTVCLK 36
DB 11 KKGKGRDL-----DDLKKEVAMTEKMSIEVCRK 41

RESULT 13
S33377
P63 protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: S33377
R:Schweizer, A.; Rohrer, J.; Jenoe, P.; DeMaio, A.; Buchman, T.G.; Hauri, H.P.
J. Cell Sci. 104, 685-694, 1993
A:Title: A reversibly palmitoylated resident protein (p63) of an ER-Colgi intermediate c
A:Reference number: S33377; MUID:93300949; PMID:8314870
A:Accession: S33377
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-601 <SCH>
A:Cross-references: EMBL:X69910; NID:9297407; PIDN:CAA49535.1; PID:g297408

Query Match 30.0%; Score 55.5; DB 2; Length 601;
Best Local Similarity 46.2%; Pred. No. 41;
Matches 12; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 2 KSGKG-KDDLRLNEIDKLWREVNSLKE 26
DB 574 ESAKGLDLDRLDLRLFLVYKVEKIH 599

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:44:09 ; Search time 6.5 Seconds
(without alignments)
229.715 Million cell updates/sec

Title: US-09-445-576A-39

Perfect score: 185

Sequence: 1 SKSGKGKDDLRNEIDKLWREVNLSKEMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	185	100.0	166	1 TETN_CARSP	P6258 carcharhinu
2	113.5	61.4	197	1 CLFL_HUMAN	O75596 homo sapien
3	89	48.1	202	1 TETN_MOUSE	P43025 mus musculus
4	84	45.4	202	1 TETN_HUMAN	P05452 homo sapien
5	60.5	32.7	488	1 K2C8_MOUSE	P11679 mus musculus
6	57	30.8	491	1 HSF1_CHICK	P38529 gallus gall
7	57	30.8	503	1 HSF1_MOUSE	P38532 mus musculus
8	57	30.8	529	1 HSF1_HUMAN	Q00613 homo sapien
9	56	30.3	547	1 BX42_DROME	P39736 drosophila
10	55.5	30.0	995	1 ALA3_CHICK	P24798 gallus gall
11	55	29.7	451	1 HSF1_HUMAN	O00291 homo sapien
12	55	29.7	451	1 HSF1_XENLA	P41154 xenopus lae
13	54.5	29.5	156	1 MAFF_MOUSE	O84791 mus musculus
14	54.5	29.5	164	1 MAFF_HUMAN	Q9uix9 homo sapien
15	54	29.2	123	1 YB44_YEAST	P38305 saccharomyc
16	53	28.6	102	1 YN16_YEAST	P48232 saccharomyc
17	53	28.6	294	1 PT54_SACBA	O13364 saccharomyc
18	53	28.6	605	1 NFL2_HUMAN	Q16236 homo sapien
19	53	28.6	1013	1 ALA3_HUMAN	P13637 homo sapien
20	52.5	28.4	241	1 RR2_FORPU	P51249 porphyra pu
21	52	28.1	229	1 RR2_ODOSI	P49490 odontella s
22	52	28.1	235	1 RR2_GUITH	O78482 guillardia
23	52	28.1	257	1 Y2G1_CAPEL	P55326 caenorhabdi
24	52	28.1	691	1 HSF1_DROME	P22813 drosophila
25	52	28.1	1286	1 CTRO_HUMAN	O14578 homo sapien
26	52	28.1	1597	1 CTRO_MOUSE	P49025 mus musculus
27	52	28.1	1679	1 Y109_YEAST	P40457 saccharomyc
28	52	28.1	2871	1 DESP_HUMAN	P15924 homo sapien
29	51.5	27.8	454	1 DNAC_BACSU	P37469 bacillus su
30	51.5	27.8	945	1 RN2_YEAST	P32565 saccharomyc
31	51	27.6	328	1 CAC_C_PEA	P17067 pisum sativ
32	51	27.6	517	1 HSF2_MOUSE	P38533 mus musculus
33	51	27.6	536	1 HSF2_HUMAN	Q03933 homo sapien

34	51	27.6	597	1 NFL2_RAT	O54968 rattus norv
35	51	27.6	1324	1 POL2_GCMV	P13026 hungarian g
36	51	27.6	1325	1 G160_MOUSE	P55937 mus musculu
37	50	27.0	233	1 RR2_GALSU	P35014 galdieria s
38	50	27.0	253	1 PSA3_SCHPO	O59770 schizosacch
39	50	27.0	291	1 RR42_HUMAN	Q15024 homo saplen
40	50	27.0	321	1 YD12_METJA	Q58708 methanococc
41	50	27.0	457	1 SYS_SULSO	O33780 sulfolobus
42	50	27.0	464	1 HOFB_HAEIN	P44622 haemophilus
43	50	27.0	468	1 K2C7_HUMAN	P08729 homo saplen
44	50	27.0	597	1 MBHL_RHOCA	P15284 rhodobacter
45	50	27.0	597	1 NFL2_MOUSE	Q60795 mus musculu

ALIGNMENTS

RESULT 1

TETN_CARSP
ID TETN_CARSP STANDARD: PRT: 166 AA.
AC P26258;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tetranectin-like protein.
OS Carcharhinus springeri (Reef shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Carcharhinidae; Carcharhinus.
OX NCBI_TaxID=7809;
RN [1]
RP SEQUENCE.
RC TISSUE=Neural arch cartilage;
RX MEDLINE=93284081; PubMed=1304877;
RA Neame P.J., Young C.N., Treep J.T.;
RT "Primary structure of a protein isolated from reef shark
(Carcharhinus springeri) cartilage that is similar to the mammalian
C-type lectin homolog, tetranectin.";
RL Protein Sci. 1:161-168(1992).
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
DR PIR: A37289; A37289.
DR HSSP; P05452; IHTN.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
DR Lectin; Cartilage.
KW DOMAIN 43 161 C-TYPE LECTIN.
FT DISULFID 37 47
FT DISULFID 64 160
FT DISULFID 136 152
SQ SEQUENCE 166 AA; 53EF812DEA5C6119 CRC64;

Query Match 100.0%; Score 185; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKSGKGKDDLRNEIDKLWREVNLSKEMQALQTVCLK 36
Db 4 SKSGKGKDDLRNEIDKLWREVNLSKEMQALQTVCLK 39

RESULT 2

CLFL_HUMAN
ID CLFL_HUMAN STANDARD: PRT: 197 AA.
AC O75596;
DT 15-JUN-2002 (Rel. 41, Created).
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-type lectin superfamily member 1 precursor (Cartilage-derived C-type
lectin).
GN CLEC3F1.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99453719; PubMed=10524194;
RA Neame P.J., Tapp H., Grimm D.R.;
RT "The cartilage-derived, C-type lectin (CLECSF1): structure of the gene
RL and chromosomal location."
RL Biochim. Biophys. Acta 1446:193-202(1999).
CC 1- TISSUE SPECIFICITY: Restricted to cartilage.
CC 1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
DR EMBL; AF077345; AAD12542.1; .
DR EMBL; AF077344; AAD12542.1; JOINED.
DR HSSP; P05452; 1HTN.
DR Genew; HGNC:2052; CLECSF1.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.
FT DOMAIN 74 192 C-TYPE LECTIN.
FT DISULFID 68 78 BY SIMILARITY.
FT DISULFID 95 191 BY SIMILARITY.
FT DISULFID 167 183 BY SIMILARITY.
FT SEQUENCE 197 AA; 22232 MW; BB924DBDB7729A4 CRC64;

Query Match 61.4%; Score 113.5; DB 1; Length 197;
Best Local Similarity 66.7%; Pred. No. 2;le-07;
Matches 22; Conservative 7; Mismatches 3; Indels 1; Gaps 1;

Qy 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
Db 38 RDKDGLKLTQIEKLWTEVNLKEIQALQTVCLR 70

RESULT 3
TETN_MOUSE STANDARD; PRT; 202 AA.
ID TETN_MOUSE
AC P43025;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=95137396; PubMed=7835708;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of a cDNA encoding murine tetranectin."
RL Gene 152:243-245(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;

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RX MEDLINE=96116955; PubMed=8563165;
RA Ibaraki R., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.;
RT "Mouse tetranectin: cDNA sequence, tissue-specific expression, and
RT chromosomal mapping."
RL Mamm. Genome 6:693-696(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=98072445; PubMed=9409787;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of the murine tetranectin gene and 5'-flanking region."
RL Gene 201:199-202(1997).
CC 1- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules destined for
CC exocytosis (By similarity).
CC 1- SUBUNIT: Homotrimer (By similarity).
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL
CC MUSCLE.
CC 1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
DR EMBL; X79199; CAA55791.1; .
DR EMBL; U08595; AAA96811.1; .
DR EMBL; X98122; CAA66804.1; .
DR HSSP; P05452; 1TN3.
DR MGD; MGI:104540; Tna.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Plasma; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 202 TETRANECTIN.
FT DOMAIN 77 198 C-TYPE LECTIN.
FT DISULFID 71 81 BY SIMILARITY.
FT DISULFID 98 197 BY SIMILARITY.
FT DISULFID 173 189 BY SIMILARITY.
FT CONFLICT 19 20 LT -> VI (IN REF. 2).
FT CONFLICT 84 84 A -> T (IN REF. 2).
FT CONFLICT 180 180 A -> R (IN REF. 2).
FT CONFLICT 188 188 R -> Q (IN REF. 2).
FT SEQUENCE 202 AA; 22257 MW; 639E7334D58EB04E CRC64;

Query Match 48.1%; Score 89; DB 1; Length 202;
Best Local Similarity 58.8%; Pred. No. 0.00026;
Matches 20; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 3 SGKGNKDLRNEIDKLWREVNSLKEMQALQTVCLK 36
Db 40 SSRKMFELKRMVDVLAQEVALLKEKQALQTVCLK 73

RESULT 4
TETN_HUMAN STANDARD; PRT; 202 AA.
ID TETN_HUMAN
AC P05452;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RT polypeptide characteristics of the type-II keratin subfamily."
RL Gene 68:109-117(1988).
CC -!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
CC KERATIN 8 ASSOCIATES WITH KERATIN 18.
CC -!- MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
CC MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC)
CC (40-55 AND 56-70 KILODALTONS, RESPECTIVELY).
CC -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CC -----
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CC -----
DR EMBL; X12789; CAA31278.1; -
DR EMBL; X15662; CAA33697.1; -
DR EMBL; M21836; AAA37550.1; -
DR EMBL; M21836; AAA37551.1; ALT_INIT.
DR PIR; S05474; S05474.
DR SWISS-2DPAGE; P11679; MOUSE.
DR MGD; MGI:96705; Krt2-8.
DR InterPro; IPR001664; IF.
DR InterPro; IPR003054; Keratin_II.
DR Pfam; PF000038; filament; 1.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Coiled coil; Keratin; Phosphorylation.
FT INT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 95 HEAD.
FT DOMAIN 96 402 ROD.
FT DOMAIN 403 488 TAIL.
FT DOMAIN 96 131 COIL 1A.
FT DOMAIN 132 148 LINKER 1.
FT DOMAIN 149 240 COIL 1B.
FT DOMAIN 241 264 LINKER 12.
FT DOMAIN 265 402 COIL 2.
FT SITE 346 346 STUTTER.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 436 436 PHOSPHORYLATION (BY MAPK AND CAMK2) (BY
FT SIMILARITY).
FT CONFLICT 189 190 QQ -> NR (IN REF. 2).
FT CONFLICT 324 324 E -> EA (IN REF. 2).
FT CONFLICT 366 366 P -> R (IN REF. 2).
SQ SEQUENCE 488 AA; 54318 MW; 9E1430800BB81523 CRC64;

Query Match 32.7%; Score 60.5; DB 1; Length 488;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 14; Conservative 8; Mismatches 7; Indels 3; Gaps 1;

QY 3 SGKGKDLR---NEIDKLRVNSLKEMQALQ 31
DB 298 AGKHGDLRRTKTEISEMNRNINRQIEALK 329

RESULT 6
HSFL_CHICK
ID HSFL_CHICK STANDARD; PRT; 491 AA.
AC P38529;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor
DE 1) (HSF 1) (HSF 3A) (HSF 3A).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Blood;
RX MEDLINE=93204945; PubMed=8455593;
RA Nakai A., Morimoto R.I.;
RT "Characterization of a novel chicken heat shock transcription factor,
RT heat shock factor 3, suggests a new regulatory pathway.";
RM Mol. Cell. Biol. 13:1983-1997(1993).
CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. HSFL IS
CC UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE HEAT SHOCKED OR
CC TREATED WITH NONTONIC DETERGENTS. IT PRESENTS CONSTITUTIVE DNA
CC BINDING ACTIVITY WHEN THE C-TERMINAL IS DELETED.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
CC TO THE NUCLEUS UPON ACTIVATION (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: LOW EXPRESSION FOUND IN MOST TISSUES WITH THE
CC EXCEPTION OF BLOOD AND LIVER. HIGHEST LEVELS ARE FOUND IN
CC PIGMENTAL LAYER OF RETINA AND IN THE LYMPHOBLASTOID CELL LINE MSB.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06098; -; NOT_ANNOTATED_CDS.
DR HSSP; P22813; 1HKT.
DR TRANSFAC; T01044; -.
DR InterPro; IPR000232; HSF_DNA_bind.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00447; HSF_DNA-bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
DR ProDom; PD001788; HSF_DNA_bind; 1.
DR SMART; SM00415; HSF; 1.
DR PROSITE; PS00434; HSF_DOMAIN; 1.
KW Transcription regulation; Nuclear protein; DNA-binding; Activator;
KW Phosphorylation; Heat shock; Multigene family.
FT DNA_BIND 20 125 BY SIMILARITY.
FT DOMAIN 135 208 HYDROPHOBIC REPEAT HR-A/B.
FT DOMAIN 346 371 HYDROPHOBIC REPEAT HR-C.
SQ SEQUENCE 491 AA; 53598 MW; D605CEB368A0B3B8 CRC64;

Query Match 30.8%; Score 57; DB 1; Length 491;
Best Local Similarity 37.1%; Pred. No. 7.4;
Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

QY 5 KGKQD-----LRNEIDKLRVNSLKEMQALQ 31
DB 153 KGQESMDSKLIAMKHNELALREVASLRQKHAQ 187

RESULT 7
HSFL_MOUSE
ID HSFL_MOUSE STANDARD; PRT; 503 AA.
AC P38532;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor
DE 1) (HSF 1).
GN HSFL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WEHI-3;
RX MEDLINE=92009180; PubMed=1717345;
RA Sarge K.D., Zimarino V., Holm K., Wu C., Morimoto R.I.;

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RT Cloning and characterization of two mouse heat shock factors with
 RL distinct inducible and constitutive DNA-binding ability.*;
 CC 5:1902-1911(1991).
 CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
 CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER
 CC EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
 CC HEAT SHOCKED.
 CC -!- SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
 CC OTHERWISE FOUND AS A MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
 CC TO THE NUCLEUS UPON ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
 CC
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 CC
 CC EMBL; X61753; CAA43892.1;
 CC PIR; A40583; A40583.
 CC HSP; P22813; LHKT.
 CC TRANSFAC; T00384;
 CC MGD; MGI:96238; Hsf1.
 CC InterPro; IPR002341; HSF_ET5.
 CC Pfam; PF00447; HSF_DNA_bind; 1.
 CC PRINTS; PR00056; HSF_DNA_BIND.
 CC PRODOM; PD001788; HSF_DNA_BIND; 1.
 CC SMART; SM00415; HSF; 1.
 CC PROSITE; PS00434; HSF_DOMAIN; 1.
 CC Transcription regulation; Nuclear protein; DNA-binding; Activator;
 KW Phosphorylation; Heat shock; Multigene family.
 FT DNA_BIND 15 120 BY SIMILARITY.
 FT DOMAIN 130 203 HYDROPHOBIC REPEAT HR-A/B.
 FT DOMAIN 380 405 HYDROPHOBIC REPEAT HR-C.
 SQ SEQUENCE 503 AA; 54930 MW; 0795ABB6FA169F7B CRC64;
 Query Match 30.8%; Score 57; DB 1; Length 503;
 Best Local Similarity 37.1%; Pred. No. 7.6;
 Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;
 OY 5 KGKDD-----LRNEIDKLRVNSLKEMQALQ 31
 DB 148 KGKQECMSKLLAMKHENALWREVASLRQKHAQQ 182
 ||| : : : : : ||||| : : : : :
 RESULT 8
 ID HSF1_HUMAN STANDARD; PRT; 529 AA.
 AC Q00613;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor
 DE 1) (HSF 1).
 GN HSF1 OR HSF1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91334376; PubMed=18711105;
 RA Rabindran S.K., Giorgi G., Clos J., Wu C.;
 RT "Molecular cloning and expression of a human heat shock factor,
 RT HSF1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:6906-6910(1991).
 RN [2]
 RP SEQUENCE OF 73-79; 81-93; 97-106; 163-170 AND 337-352.

RX MEDLINE=91334377; PubMed=18711106;
 RA Schuetz T.J., Gallo G.J., Sheldon L., Tempst P., Kingston R.E.;
 RT "Isolation of a cDNA for HSF2: evidence for two heat shock factor
 RT genes in humans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:6911-6915(1991).
 CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
 CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER
 CC EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
 CC HEAT SHOCKED.
 CC -!- SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
 CC OTHERWISE FOUND AS A MONOMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
 CC TO THE NUCLEUS UPON ACTIVATION.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
 CC
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 CC
 CC EMBL; M64673; AAA52695.1;
 CC PIR; A41137; A41137.
 CC HSP; P22813; LHKT.
 CC TRANSFAC; T01042;
 CC Genew; HGNC:5224; HSF1.
 CC MIM; 140580;
 CC InterPro; IPR002342; HSF_DNA_bind.
 CC InterPro; IPR002341; HSF_ET5.
 CC Pfam; PF00447; HSF_DNA_bind; 1.
 CC PRINTS; PR00056; HSF_DOMAIN.
 CC PRODOM; PD001788; HSF_DNA_BIND; 1.
 CC SMART; SM00415; HSF; 1.
 CC PROSITE; PS00434; HSF_DOMAIN; 1.
 CC Transcription regulation; Nuclear protein; DNA-binding; Activator;
 KW Phosphorylation; Heat shock; Multigene family; Alternative splicing.
 FT DNA_BIND 15 120 BY SIMILARITY.
 FT DOMAIN 130 203 HYDROPHOBIC REPEAT HR-A/B.
 FT DOMAIN 384 409 HYDROPHOBIC REPEAT HR-C.
 FT VARSPLIC 462 489 GKQLVHYTAQPLFLDPLGSDVTGSNDLP -> AGALHSAAA
 FT VARSPLIC 490 529 VPAGPLRGHRQRPAQAV (IN SHORT ISOFORM).
 SQ SEQUENCE 529 AA; 57260 MW; 735074507C954365 CRC64;
 Query Match 30.8%; Score 57; DB 1; Length 529;
 Best Local Similarity 37.1%; Pred. No. 8.1;
 Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;
 OY 5 KGKDD-----LRNEIDKLRVNSLKEMQALQ 31
 DB 148 KGKQECMSKLLAMKHENALWREVASLRQKHAQQ 182
 ||| : : : : : ||||| : : : : :
 RESULT 9
 ID BX42_DROME STANDARD; PRT; 547 AA.
 AC P39736;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Puff specific protein Bx42.
 GN BX42.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-Oregon-R; TISSUE=Embryo;
RA MEDLINE=93048378; PubMed=1424996;
RX Wieland C., Mann S., von Besser H., Saumweber H.;
RT "The Drosophila nuclear protein Bx42, which is found in many puffs on
RL polytene chromosomes, is highly charged.";
RL Chromosome 101:517-525(1992).
CC -1- FUNCTION: MAY PLAY A ROLE IN CHROMATIN STRUCTURE AND FUNCTION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: TWO TRANSCRIPTS ARE DETECTED OF SIZES 1.9 AND
CC 2.2 KB. BOTH ARE DETECTED SOON AFTER FERTILIZATION AND SHOW
CC RELATIVELY CONSTANT EXPRESSION DURING THE FIRST 2/3 OF
CC EMBRYOGENESIS. IN 0-3 HR EMBRYOS, THE SMALLER TRANSCRIPT IS
CC PREDOMINANT AND THE LEVELS OF THE TWO TRANSCRIPTS ARE SOMEWHAT
CC REDUCED AT THE LATER STAGES OF DEVELOPMENT, BUT THEY ARE FOUND
CC APPROXIMATELY CONSTANT AMOUNTS DURING LARVAL, PUPAL AND ADULT
CC STAGES. THE SMALLER TRANSCRIPT IS SUSPECTED TO BE A MATERNAL
CC TRANSCRIPT.
CC -1- SIMILARITY: BELONGS TO THE SNW FAMILY.
CC -----
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CC -----
CC EMBL: X64536; CAA45834.1; -
CC FlyBase: FBgn0004856; Bx42.
CC InterPro: IPR004015; SKIP_SNW.
CC Pfam: PF02731; SKIP_SNW; 1.
CC Nuclear protein; DNA-binding.
CC FT DOMAIN 177 343 SNW
CC FT DOMAIN 383 462 SH2-LIKE DOMAIN.
CC FT DOMAIN 209 236 PRO-RICH.
CC FT DOMAIN 125 155 ASP/GLU-RICH (ACIDIC).
CC FT DOMAIN 300 400 ASP/GLU-RICH (ACIDIC).
CC SEQUENCE 547 AA; 61156 MW; 01399EA291C9D557 CRC64;
CC -----
CC Query Match 30.3%; Score 56; DB 1; Length 547;
CC Best Local Similarity 50.0%; Pred. No. 11;
CC Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
CC
CC QY 3 SGKGDDLRNEIDKLRVNSL 24
CC |||||:|:|:|:|:|:|:
CC Db 431 SGYGDDEAYNVYDKPRDNTL 452
CC
CC RESULT 10
CC ID A1A3_CHICK STANDARD; PRT; 1010 AA.
CC AC P24798;
CC DT 01-MAR-1992 (Rel. 21, Created)
CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9)
CC DE (Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
CC GN A1P1A3.
CC OS Gallus gallus (Chicken).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91023019; PubMed=2171348;
CC RA Takeyasu K., Lemas V., Fambrough D.M.;
CC RT "Stability of Na(+)-K(+)-ATPase alpha subunit isoforms in evolution.";
CC RL Am. J. Physiol. 259:C619-C630(1990).
CC CC -1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
CC WHICH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF
CC NA AND K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
CC ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR

CC ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) -> ADP +
CC phosphate + Na(+)(Out) + K(+)(In).
CC -1- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
CC AND GAMMA.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). SUBFAMILY IIC.
CC -----
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CC -----
CC EMBL: M59960; AAA48982.1; -
CC PIR: B37227; B37227.
CC HSP: P04191; 1EUL.
CC InterPro: IPR001757; ATPase_E1-E2.
CC InterPro: IPR004014; Cation_ATPase.
CC InterPro: IPR000661; H/K_Na/K_ATPase.
CC InterPro: IPR001454; Hlgnaase/hydriase.
CC Pfam: PF00122; E1-E2_ATPase; 1
CC Pfam: PF00689; Cation_ATPase_C; 1.
CC Pfam: PF00690; Cation_ATPase_N; 1.
CC Pfam: PF00702; Hydriase; 1.
CC PRINTS: PR00119; CATATPASE.
CC PRINTS: PR00121; NAKATPASE.
CC TIGRFAMs: TIGR01106; X_K_ATPasealp; 1.
CC PROSITE: PS00154; ATPase_E1_E2; 1
CC Hydriase; Sodium/potassium transport; Transmembrane; Phosphorylation;
CC Magnesium; Metal-binding; ATP-binding; Multigene family.
CC FT DOMAIN 1 74 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 75 95 POTENTIAL.
CC FT DOMAIN 96 118 LUMENAL (POTENTIAL).
CC FT TRANSMEM 119 139 POTENTIAL.
CC FT DOMAIN 140 275 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 276 295 POTENTIAL.
CC FT DOMAIN 296 307 LUMENAL (POTENTIAL).
CC FT TRANSMEM 308 325 POTENTIAL.
CC FT DOMAIN 326 759 POTENTIAL.
CC FT TRANSMEM 760 779 POTENTIAL.
CC FT DOMAIN 780 789 LUMENAL (POTENTIAL).
CC FT TRANSMEM 790 810 LUMENAL (POTENTIAL).
CC FT DOMAIN 811 830 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 831 853 POTENTIAL.
CC FT DOMAIN 854 905 LUMENAL (POTENTIAL).
CC FT TRANSMEM 906 925 POTENTIAL.
CC FT DOMAIN 926 938 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 939 957 POTENTIAL.
CC FT DOMAIN 958 972 LUMENAL (POTENTIAL).
CC FT TRANSMEM 973 993 POTENTIAL.
CC FT DOMAIN 994 1010 CYTOPLASMIC (POTENTIAL).
CC FT MOD_RES 363 363 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 930 930 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC FT BINDING 69 71 BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
CC SIMILARITY).
CC FT METAL 704 704 MAGNESIUM (BY SIMILARITY).
CC FT METAL 708 708 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 1010 AA; 111284 MW; 71526BC25633BFA6 CRC64;
CC -----
CC Query Match 30.3%; Score 56; DB 1; Length 1010;
CC Best Local Similarity 40.0%; Pred. No. 22;
CC Matches 14; Conservative 5; Mismatches 12; Indels 4; Gaps 1;
CC
CC QY 2 KSGKGDDLRNEIDKLRVNSLKEQALQTVCLK 36
CC |||||:|:|:|:|:|:|:
CC Db 11 KKGKGRDL-----DDLAKVAMTEHKMSIEVCCK 41
CC
CC RESULT 11

HIPL_HUMAN
ID HIPL_HUMAN STANDARD; PRT; 995 AA.
AC 000291; 000328;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Huntingtin interacting protein 1 (HIP-1) (Fragment).
GN HIPL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huq A.H.M., Nichol K., Osborne L., Scherer S.W., Squitieri F.,
RT Hayden M.R.;
RT "Genomic organization of the human HIPL gene and its exclusion as a
RT candidate gene in a family diagnosed with Huntington disease without
RT CAG expansion.";
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 82-995 FROM N.A.
RX MEDLINE=97285121; PubMed=9140394;
RA Kalchman M.A., Koide H.B., McCutcheon K., Graham R.K., Nichol K.,
RA Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C.,
RA Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M.R.;
RT "HIP-1, a human homologue of S. cerevisiae Sla2p, interacts with
RT membrane-associated huntingtin in the brain.";
RL Nat. Genet. 16:44-53(1997).
RN [3]
RP SEQUENCE OF 82-159 FROM N.A.
RA Bradshaw H., Hinds K., Harrison M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 203-602 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97227296; PubMed=9147654;
RA Wanker E.E., Kovira C., Scherzinger E., Hasenbank R., Waelter S.,
RA Tait D., Colicelli J., Lehrach H.;
RT "HIP-1: a huntingtin interacting protein isolated by the yeast two-
RT hybrid system.";
RL Hum. Mol. Genet. 6:487-495(1997).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=2051263; PubMed=11063258;
RA Chopra V.S., Metzler M., Rasper D.M., Engqvist-Goldstein A.E.Y.,
RA Singaraja R., Gan L., Fichter K.M., McCutcheon K., Drubin D.,
RA Nicholson D.W., Hayden M.R.;
RT "HIP2 is a non-proapoptotic member of a gene family including HIP1,
RT an interacting protein with huntingtin.";
RL Mamm. Genome 11:1006-1015(2000).
CC -!- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE CELL FILAMENT
CC NETWORKS.
CC -!- SUBUNIT: BINDS HUNTINGTIN. THIS INTERACTION IS RESTRICTED TO THE
CC BRAIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. MEMBRANE-ASSOCIATED PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED
CC BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH THE HIGHEST LEVEL
CC IN BRAIN.
CC -!- MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIPL
CC INTERACTION IS INVERSELY CORRELATED TO THE LENGTH OF THE
CC POLYGLUTAMINE TRACT ADDED TO THE HUNTINGTIN PROTEIN IN HUNTINGTON
CC DISEASE.
CC -!- SIMILARITY: BELONGS TO THE SLA2 FAMILY.
CC
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CC
DR EMBL; AF052288; AAC33564.1; JOINED.
DR EMBL; AF052261; AAC33564.1; JOINED.
DR EMBL; AF052262; AAC33564.1; JOINED.
DR EMBL; AF052263; AAC33564.1; JOINED.
DR EMBL; AF052264; AAC33564.1; JOINED.
DR EMBL; AF052265; AAC33564.1; JOINED.
DR EMBL; AF052266; AAC33564.1; JOINED.
DR EMBL; AF052267; AAC33564.1; JOINED.
DR EMBL; AF052268; AAC33564.1; JOINED.
DR EMBL; AF052269; AAC33564.1; JOINED.
DR EMBL; AF052270; AAC33564.1; JOINED.
DR EMBL; AF052271; AAC33564.1; JOINED.
DR EMBL; AF052272; AAC33564.1; JOINED.
DR EMBL; AF052273; AAC33564.1; JOINED.
DR EMBL; AF052274; AAC33564.1; JOINED.
DR EMBL; AF052275; AAC33564.1; JOINED.
DR EMBL; AF052276; AAC33564.1; JOINED.
DR EMBL; AF052277; AAC33564.1; JOINED.
DR EMBL; AF052278; AAC33564.1; JOINED.
DR EMBL; AF052279; AAC33564.1; JOINED.
DR EMBL; AF052280; AAC33564.1; JOINED.
DR EMBL; AF052281; AAC33564.1; JOINED.
DR EMBL; AF052282; AAC33564.1; JOINED.
DR EMBL; AF052283; AAC33564.1; JOINED.
DR EMBL; AF052284; AAC33564.1; JOINED.
DR EMBL; AF052285; AAC33564.1; JOINED.
DR EMBL; AF052286; AAC33564.1; JOINED.
DR EMBL; AF052287; AAC33564.1; JOINED.
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RN  SEQUENCE FROM N.A.
RP  MEDLINE=95369690; Pubmed=7642097;
RA  Stump D.G., Landsberger N., Wolffe A.P.;
RT  "The cDNA encoding Xenopus laevis heat-shock factor 1 (XHSF1):
RT  nucleotide and deduced amino-acid sequences, and properties of the
RT  encoded protein.";
RL  Gene 160:207-211(1995).
CC  -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC  PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
CC  SIMILARITY).
CC  -!- SUBUNIT: HOMODIMER.
CC  -!- SUBCELLULAR LOCATION: Nuclear.
CC  -!- PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
CC  (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC  -----
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CC  -----
DR  EMBL; L36924; AAA99999.1; -
DR  HSSP; P22813; IHKT.
DR  TRANSFAC; T01041; -
DR  InterPro; IPR000232; HSF_DNA_bind.
DR  Pfam; PF00447; HSF_DNA-bind; 1.
DR  PRINTS; PR00056; HSFDOMAIN.
DR  ProDom; PD001788; HSF_DNA_bind; 1.
DR  SMART; SM00415; HSF; 1.
DR  PROSITE; PS00434; HSF_DOMAIN; 1.
KW  Transcription regulation; Nuclear protein; DNA-binding; Activator;
KW  Phosphorylation; Heat shock.
FT  DNA_BIND 12 117
FT  SEQUENCE 451 AA; 49472 MW; 3E271549BCABB10 CRC64;
SQ
Query Match 29.7%; Score 55; DB 1; Length 451;
Best Local Similarity 34.2%; Pred. No. 12;
Matches 13; Conservative 8; Mismatches 9; Indels 8; Gaps 1;

QY  2 KSCGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
Db  142 QSMKGQESIDGRLLSMKHNEALWREVASLRQKHTQQ 179
      :| ||| : : : : | ||| | : : |
      :| ||| : : : : | ||| | : : |

RESULT 13
MAFF_MOUSE
ID  MAFF_MOUSE STANDARD; PRT; 156 AA.
AC  Q54791;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Transcription factor MaF (V-maf musculoaponeurotic fibrosarcoma
DE  oncogene homolog F).
GN  MAFF.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
RC  STRAIN=129/SVJ;
RX  Pubmed=10409670;
RA  Onodera K., Shavit J.A., Motohashi H., Katsuoaka F., Akasaka J.-E.,
RA  Engel J.D., Yamamoto M.;
RT  "Characterization of the murine maff gene.";
RL  J. Biol. Chem. 274:21162-21169(1999).
RN  [2]
RP  SEQUENCE FROM N.A.

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```

RC  TISSUE=Liver;
RA  Strausberg R.;
RL  Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Interacts with the upstream promoter region of the
CC  oxytocin receptor gene. May be a transcriptional enhancer in the
CC  upregulation of the oxytocin receptor gene at parturition. Since
CC  it lacks a putative transactivation domain, it may behave as a
CC  transcriptional repressor when it dimerize among himself. May also
CC  serve as a transcriptional activator by dimerizing with other
CC  (usually larger) basic-zipper proteins and recruiting them to
CC  specific DNA-binding sites. May be involved in the cellular stress
CC  response.
CC  -!- SUBUNIT: Monomer and homo- or heterodimer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC  -!- TISSUE SPECIFICITY: Highly expressed in the lung, lower expression
CC  in the brain, thymus, liver, spleen, intestine, kidney, heart,
CC  muscle, and ovary. Not significantly expressed in hematopoietic
CC  cells.
CC  -!- DEVELOPMENTAL STAGE: Detected at 6.5 dpc, in the boundary between
CC  the extraembryonic and embryonic regions. At 8.5 dpc, weakly
CC  expressed in the furor gut, allantois, yolk sac endoderm and the
CC  ectoplacental cone. At 9.5 dpc, strong expression in the
CC  primordial gut and presumptive fetal liver, in the floorplate of
CC  the myelencephalon, neural crest cells, spongiotrophoblasts, and
CC  giant cells of the placenta. At 12.5 dpc, detected in hepatocytes,
CC  in the outflow tract of the heart in a specific subset of dorsal
CC  root ganglia, in the cranial nerve ganglia, in the lung
CC  primordium, and in the epithelium of the expiratory tract. In
CC  bronchial epithelia, and bone membrane.
CC  -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AB009694; BAA24029.1; -
DR  EMBL; BC022952; AAH22952.1; -
DR  MGD; MGI:96910; Maff.
DR  InterPro; IPR004827; TF_BZIP.
DR  InterPro; IPR004826; TF_Maf.
DR  Pfam; PF03131; BZIP_Maf; 1.
DR  SMART; SM00338; BRLZ; 1.
KW  Transcription regulation; DNA-binding; Repressor; Nuclear protein.
FT  DNA_BIND 53 83
FT  DOMAIN 86 114
FT  BASIC MOTIF.
FT  LEUCINE-ZIPPER.
SQ  SEQUENCE 156 AA; 16954 MW; 574DD05499819037 CRC64;

Query Match 29.5%; Score 54.5; DB 1; Length 156;
Best Local Similarity 41.9%; Pred. No. 4.3;
Matches 13; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY  5 KKDLDLRNIDKLWREVNSLK-EMQALQTVQ 34
Db  81 KOKSELEREVDKLARENAMRLDLAGKGC 111
      | | | | | | | | : : | | |
      | | | | | | | | : : | | |

RESULT 14
MAFF_HUMAN
ID  MAFF_HUMAN STANDARD; PRT; 164 AA.
AC  Q9ULX9; Q9Y525;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Transcription factor MaF (V-maf musculoaponeurotic fibrosarcoma
DE  oncogene homolog F) (U-Maf).
GN  MAFF.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


RT "RIM2, MS11 and PG11 are located within an 8 kb segment of
RT Saccharomyces cerevisiae chromosome II, which also contains the
RT putative ribosomal gene L21 and a new putative essential gene with a
RT leucine zipper motif.";
RL Yeast 9:645-659(1993).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z21487; CAA79681.1; -;
DR EMBL; Z36063; CAA85156.1; -;
DR PIR; S34019; S34019.
DR SGD; S0000398; YBR194W.
KW Hypothetical protein.
SQ SEQUENCE 123 AA; 14234 MW; AF25FE81D22D4C8C CRC64;

Query Match 29.2%; Score 54; DB 1; Length 123;
Best Local Similarity 44.4%; Pred. No. 3.9;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 7 KDDLREIDKLWREVNLSKEMQALQTV 33
| :|:::| | : |||
Db 24 KKYVRNQVESLSRLNRNKEGQLQTV 50

Search completed: April 15, 2003, 11:48:35
Job time : 7.5 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:44:50 ; Search time 22.5 Seconds
(without alignments)
329.675 Million cell updates/sec

Title: US-09-445-576A-39

Perfect score: 185

Sequence: 1 SKSGKGKDLRNEIDKLWREVNSLKEMQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	128	69.2	196	11	Q9EPW4	Q9epw4 mus musculus
2	124.5	67.3	197	6	Q28008	Q28008 bos taurus
3	86	46.5	201	13	Q9DDA4	Q9ddd4 gallus gall
4	65	35.1	478	13	Q98TQ7	Q98tq7 lampetra fl
5	62	33.5	1040	2	Q8RTE4	Q8rte4 campylobact
6	61	33.0	1040	16	Q9PID6	Q9pid6 campylobact
7	60	32.4	1105	10	Q949K1	Q949k1 lycopersico
8	59	31.9	324	17	Q96Z84	Q96z84 sulfolobus
9	59	31.9	582	16	Q67141	Q67141 aquifex aeo
10	58.5	31.6	233	16	Q8RFV0	Q8rfv0 fusobacteri
11	57.5	31.1	103	4	Q75215	Q75215 homo sapien
12	57.5	31.1	461	5	Q77390	Q77390 plasmodium
13	57	30.8	448	11	Q63717	Q63717 rattus norv
14	57	30.8	486	11	Q70462	Q70462 mus musculus
15	57	30.8	912	2	Q9LA12	Q9lai2 bacillus sp
16	57	30.8	1191	11	P97690	P97690 rattus norv

17	57	30.8	1217	4	O60464	O60464 homo sapien
18	57	30.8	1217	11	Q9QUS3	Q9qus3 mus musculus
19	57	30.8	1218	6	Q97594	Q97594 bos taurus
20	56.5	30.5	348	13	O57378	O57378 gallus gall
21	56.5	30.5	466	11	Q8R3F2	Q8r3f2 mus musculus
22	56	30.3	120	5	Q8ST11	Q8st11 plasmodium
23	56	30.3	281	17	Q9V217	Q9v217 pyrococcus
24	56	30.3	862	6	Q9BE52	Q9be52 macaca fasc
25	56	30.3	917	5	Q9VBX5	Q9vbx5 drosophila
26	55.5	30.0	560	4	Q8TB01	Q8tb01 homo sapien
27	55.5	30.0	602	4	Q07065	Q07065 homo sapien
28	55.5	30.0	1030	4	Q8TDL4	Q8tdl4 homo sapien
29	55	29.7	225	13	Q9IB42	Q9ib42 paralicthy
30	55	29.7	225	13	Q9IB41	Q9ib41 paralicthy
31	55	29.7	401	5	Q9VD71	Q9vd71 drosophila
32	55	29.7	559	12	Q9Q8U5	Q9q8u5 shope fibro
33	55	29.7	559	12	Q90026	Q90026 rabbit fibr
34	55	29.7	635	16	Q99Q22	Q99q22 staphylococ
35	55	29.7	666	10	Q8S604	Q8s604 oryza sativ
36	55	29.7	687	10	Q8S775	Q8s775 oryza sativ
37	55	29.7	836	5	O44490	O44490 caenorhabdi
38	55	29.7	974	10	Q94CG5	Q94cg5 petunia int
39	54.5	29.5	152	2	Q9RN31	Q9rn31 bacillus an
40	54.5	29.5	198	2	Q9RN29	Q9rn29 bacillus an
41	54	29.2	232	17	Q9UXI5	Q9uxi5 sulfolobus
42	54	29.2	690	5	Q94379	Q94379 caenorhabdi
43	54	29.2	799	4	Q94874	Q94874 homo sapien
44	53.5	28.9	353	5	O17609	O17609 caenorhabdi
45	53.5	28.9	353	5	O02226	O02226 caenorhabdi

ALIGNMENTS

RESULT 1

Q9EPW4 ID Q9EPW4 PRELIMINARY; PRT; 196 AA.
AC Q9EPW4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE C-type lectin superfamily 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES129/SV;
RA Neame P.J., Grimm D.R.;
RT "Mouse homolog of human CLCFSF1, a cartilage derived C-type lectin.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317204; AAG48620.1;
DR HSSP; P05452; IHTN.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;
Query Match 69.2%; Score 128; DB 11; Length 196;
Best Local Similarity 75.9%; Pred. No. 3.2e-08;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36

Db 42 DDLKSQVEKLWREVNALKEMQALQTVCLR 70

RESULT 2

Q28008

ID Q28008 PRELIMINARY; PRT; 197 AA.
AC Q28008;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-type lectin homolog precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARTILAGE;
RA Neame P.J., Boynton R.E.;
RT "C-type lectin homolog from bovine cartilage."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; P05298; AAC18614.1; -;
DR HSSP; P05452; 1TN3.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 197 C-TYPE LECTIN HOMOLOG.
FT SEQUENCE 197 AA; 22215 MW; AAC4280F41AC0F4 CRC64;
Query Match 67.3%; Score 124.5; DB 6; Length 197;
Best Local Similarity 72.7%; Pred. No. 8.9e-08;
Matches 24; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
QY 5 KGKD-DLRNEIDKLWREVNLSKEMQALQTVCLK 36
Db 38 KEKGDGLKTQVEKLWREVNLSKEMQALQTVCLK 70
RESULT 3
Q9DD04 PRELIMINARY; PRT; 201 AA.
AC Q9DD04;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tetranectin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Wewer U.M.;
RT "tetranectin in chicken."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277116; CAC20217.1; -;
DR HSSP; P05452; 1TN3.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 1.
DR SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;
Query Match 46.5%; Score 86; DB 13; Length 201;
Best Local Similarity 41.2%; Pred. No. 0.0053;
Matches 21; Conservative 7; Mismatches 7; Indels 16; Gaps 1;
QY 2 KSGKGK-----DLRNEIDKLWREVNLSKEMQALQTVCLK 36
Db 22 QNGKGKGRPAASKGDKGSLKMLIEDLKAMIDNISQEVALLKEKQALQTVCLK 72

RESULT 4
Q98TQ7 PRELIMINARY; PRT; 478 AA.
AC Q98TQ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Keratin type II Lfi-K 1.
GN KERATIN.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RA Schultess J., Schaffeld M., Markl J.;
RT "Type II keratin; intermediate filament protein from Lampetra fluviatilis."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
DR EMBL; AJ401159; CAC24702.1; -;
DR InterPro: IPR001664; IF.
DR InterPro: IPR002957; Keratin_I.
DR Pfam: PF00038; filament; 1.
DR PRINTS; PR01248; TYPE1KERATIN.
DR PRINTS; PR01276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Coiled coil; Intermediate filament.
SQ SEQUENCE 478 AA; 51130 MW; A7A16BDC57AB9D41 CRC64;
Query Match 35.1%; Score 65; DB 13; Length 478;
Best Local Similarity 45.7%; Pred. No. 5.3;
Matches 16; Conservative 10; Mismatches 5; Indels 4; Gaps 2;
QY 1 SKSGKGKDDL---RNEIDKLWREVNLSK-EMQALQ 31
Db 302 SSAGKGDDDDVRNSRNEINELNQMORIKAEIALK 336
RESULT 5
Q98TE4 PRELIMINARY; PRT; 1040 AA.
AC Q98TE4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CmeB.
GN CMEB.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=81-176;
RA Lin J., Michel L.O., Zhang Q.;
RT "CmeABC functions as a multidrug efflux system in Campylobacter jejuni."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466820; AAL74245.1; -;
DR SEQUENCE 1040 AA; 113962 MW; 8A8D50F09F2B69BE CRC64;
Query Match 33.5%; Score 62; DB 2; Length 1040;
Best Local Similarity 34.4%; Pred. No. 28;
Matches 11; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 SKSGKGKDDLRLNEIDKLWREVNLSKEMQALQ 32
Db 681 NKSGKSYDEIQKDVNKNLVAANQORKELSRVT 712

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RESULT 6
Q9PID6 ID Q9PID6 PRELIMINARY; PRT; 1040 AA.
AC Q9PID6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transmembrane efflux protein.
GN CJO366C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL; ALJ39075; CAB74202.1;
DR InterPro; IPR001036; Acrlflvin_res.
DR InterPro; IPR004764; HAEI.
DR InterPro; IPR000731; HMGCR/patch_5TM.
DR Pfam; PF00873; ACR_tran; 1.
DR PRINTS; PR00702; ACRIFLAVINRP.
DR TIGRFAMS; TIGR00915; 2A0602; 1.
DR PROSITE; PS50156; SSD; 2.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 1040 AA; 113966 MW; 022005EDA20BE4C4 CRC64;

Query Match 33.0%; Score 61; DB 16; Length 1040;
Best Local Similarity 34.4%; Pred. No. 37;
Matches 11; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 1 SKSGKGDDLRNEIDKLRVNSLKEMQALOT 32
Db 681 NKSRSYDEIQKVNKLAVANQRKLSRVRT 712

RESULT 7
Q949K1 ID Q949K1 PRELIMINARY; PRT; 1105 AA.
AC Q949K1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 126.2 kDa protein.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HEINZ 1706; TRANSPOSOM=FOLDBACK TRANSPOSOM TAPIR1;
RX MEDLINE=20426111; PubMed=10972295;
RA Mao L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,
RA Irish E.E., Wing R.A.;
RA "JOINTLESS is a MADS-box gene controlling tomato flower abscission
RT zone development."
RT Nature 406:910-913(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HEINZ 1706; TRANSPOSOM=FOLDBACK TRANSPOSOM TAPIR1;
RX MEDLINE=21351421; PubMed=11457984;
RA Mao L., Begum D., Goff S.A., Wing R.A.;
RA "Sequence and analysis of the tomato jointless locus."
RT

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RL Plant Physiol. 126:1331-1340(2001).
DR EMBL; AF275345; AAK84476.1;
KW Hypothetical protein.
SQ SEQUENCE 1105 AA; 126205 MW; C28E3A45B6201EF4 CRC64;

Query Match 32.4%; Score 60; DB 10; Length 1105;
Best Local Similarity 48.1%; Pred. No. 53;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 KSGKGKDDLRNEIDKLRVNSLKEMQ 28
Db 341 KSLTKDEALEEIDKLRDILSLQTVK 367

RESULT 8
Q96284 ID Q96284 PRELIMINARY; PRT; 324 AA.
AC Q96284;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein ST1947.
GN ST1947.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7."
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000988; BAB67042.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 324 AA; 37895 MW; 3E0F5C5876ED4244 CRC64;

Query Match 31.9%; Score 59; DB 17; Length 324;
Best Local Similarity 57.9%; Pred. No. 19;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 8 DDLRNEIDKLRVNSLKE 26
Db 213 EKLNEIDKLRKEINDLKD 231

RESULT 9
O67141 ID O67141 PRELIMINARY; PRT; 582 AA.
AC O67141;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Elongation factor SELB.
OS SELB OR AQ_1033.
GN Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujaay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT

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RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
DR EMBL; AE000719; AAC07099.1; -.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; EF-GTPbind.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR004535; TEF_SelB.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR TIGRFAMs; TIGR00475; selB; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW Elongation factor; GTP-binding; Complete proteome.
SQ SEQUENCE 582 AA; 66174 MW; EF4BF3D94AA002BC CRC64;

Query Match 31.9%; Score 59; DB 16; Length 582;
Best Local Similarity 37.9%; Pred. No. 36;
Matches 11; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 3 SGKGDLLRNEIDKLWREVNSLKEMQALQ 31
Db 153 TGOGIEDLKNISIKLLESINNLRHKPLR 181

RESULT 10
Q8RFV0 PRELIMINARY; PRT; 233 AA.
ID Q8RFV0;
AC Q8RFV0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lipoprotein releasing system ATP-binding protein 10LD.
GN FN0582.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21886394; PubMed=11889109;
RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010570; AAL94778.1; -.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 233 AA; 26805 MW; D2D8AE692B2D356F CRC64;

Query Match 31.6%; Score 58.5; DB 16; Length 233;
Best Local Similarity 44.7%; Pred. No. 16;
Matches 17; Conservative 5; Mismatches 5; Indels 11; Gaps 3;

QY 2 KSGKGDDLRLN-----EID--KLW---REVNSLKEMQ 28
Db 51 KSGSGKSTLLNGLDKIDGGKIWDKREVSLSNEME 88

RESULT 11
ID 075215 PRELIMINARY; PRT; 103 AA.
AC 075215;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE WUGSC:H.DJ0870F17.1 protein (Fragment).
GN WUGSC:H.DJ0870F17.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer C., Langston Y., Harrison M., Lennox S.;
RT "The sequence of Homo sapiens PAC clone RP5-870F17."
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004911; AAC33151.1; -.
DR InterPro; IPR000531; TonB_box.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11347 MW; EE712650E3109C76 CRC64;

Query Match 31.1%; Score 57.5; DB 4; Length 103;
Best Local Similarity 42.4%; Pred. No. 8.9;
Matches 14; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 3 SGKG-KDDLRLNEIDKLWREVNSLKEMQALQTV 34
Db 67 STKGLDLDLKNLDGLFVEVEKIYVNSMNCV 99

RESULT 12
ID 077390 PRELIMINARY; PRT; 461 AA.
AC 077390;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 54.7 kDa protein.
GN PFC0720W, MAJ3P6.5.
OS Plasmidium faiciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Hassall B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT faiciparum."
RL Nature 400:532-538(1999).
DR EMBL; Z98551; CAB11146.2; -.
KW Hypothetical protein.
SQ SEQUENCE 461 AA; 54677 MW; 6A33BEC7628758C5 CRC64;

Query Match 31.1%; Score 57.5; DB 5; Length 461;
Best Local Similarity 28.9%; Pred. No. 43;
Matches 11; Conservative 13; Mismatches 7; Indels 7; Gaps 1;

QY 6 GKDDLRLNEIDKLWREVN-----SLKEMQALQTVCLK 36
Db 16 GFEMRNEMNRYGVEINQSTLKNPSTEDIQIYSLCIK 53

RESULT 13
ID 063717 PRELIMINARY; PRT; 448 AA.
AC 063717;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heat shock transcription factor 1 (Fragment).
```

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GN HSFL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=LIVER;
RA Swamynathan S.K., Revathi C.J., Srinivas U.K.;
RT "Cloning and characterization of rat heat shock transcription factor
  1.";
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X83094; CAA58149.1; -
DR HSP; P22813; IHKT.
DR InterPro; IPR000232; HSF_DNA_bind.
DR Pfam; PF00447; HSF_DNA_bind; 1.
DR ProDom; PD001788; HSF_DNA_bind; 1.
DR SMART; SM00415; HSF; 1.
FT NON_TER 1
SQ SEQUENCE 448 AA; 48719 MW; CE615F42DBA759D8 CRC64;

Query Match 30.8%; Score 57; DB 11; Length 448;
Best Local Similarity 37.1%; Pred. No. 48;
Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

QY 5 KGKDD-----LRNEIDKLRVNSLKEMOALQ 31
   ||| : : : : ||||| ||: : |
Db 71 KGKQECMDSKLLAMKHENEALWREVASLRQKHAQQ 105

RESULT 14
O70462
ID O70462 PRELIMINARY; PRT; 486 AA.
AC O70462;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Heat shock transcription factor 1 (Fragment).
RL J. Biol. Chem. 273:32514-32521(1998).
DR EMBL; AF059275; AAC80425.1; -
DR HSP; P22813; IHKT.
DR MGD; MGI:96238; HSfl.
DR InterPro; IPR000232; HSF_DNA_bind.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00447; HSF_DNA_bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
DR ProDom; PD001788; HSF_DNA_bind; 1.
DR SMART; SM00415; HSF; 1.
DR PROSITE; PS00434; HSF_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 486 AA; 53213 MW; EE164394C51D9DF7 CRC64;

Query Match 30.8%; Score 57; DB 11; Length 486;
Best Local Similarity 37.1%; Pred. No. 52;
Matches 13; Conservative 7; Mismatches 7; Indels 8; Gaps 1;

QY 5 KGKDD-----LRNEIDKLRVNSLKEMOALQ 31
   ||| : : : : ||||| ||: : |
Db 109 KGKQECMDSKLLAMKHENEALWREVASLRQKHAQQ 143
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RESULT 15
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ID Q9LAI2 PRELIMINARY; PRT; 912 AA.
AC Q9LAI2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE BSLIM.
GN BSLIM.
OS Bacillus sp. NEB-606.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=114630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ENGLAND BIOLAB #606;
RX MEDLINE=20115537; PubMed=10648519;
RA Hsieh P.C., Xiao J.P., O'Loane D., Xu S.Y.;
RT "Cloning, Expression, and Purification of a Thermostable
  Nonhomodimeric Restriction Enzyme, BslI.";
RL J. Bacteriol. 182:949-955(2000).
DR EMBL; AF135191; AAF32529.1; -
DR InterPro; IPR001091; CM4_Mettransf.
DR InterPro; IPR002295; D2IN6_mtfrase.
DR Pfam; PF01555; N6_N4_Mtase; 1.
DR PRINTS; PR00506; D2IN6MTFRASE.
DR PRINTS; PR00508; S2IN4MTFRASE.
DR PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
SQ SEQUENCE 912 AA; 107438 MW; 8FF7F1F86102C25 CRC64;

Query Match 30.8%; Score 57; DB 2; Length 912;
Best Local Similarity 37.9%; Pred. No. 1e+02;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 7 KDDLREIDKLRVNSLKEMOALQTVCL 35
   | : || ||| | : | : |
Db 130 KEKIKNEFIKLWNEANEVNEYGKLDYLL 158

Search completed: April 15, 2003, 11:50:17
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:41:29 ; Search time 14 Seconds
(without alignments)
380.396 Million cell updates/sec

Title: US-09-445-576A-7

Perfect score: 960
Sequence: 1 EPTQPKKIVNAKDVNT.....KWFDKRCRDLPYICQFIV 181

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	960	100.0	202	1	US-08-469-486-56
2	960	100.0	202	2	US-08-469-486-56
3	422.5	44.0	197	4	US-09-602-877A-99
4	186.5	19.4	1257	1	US-08-340-4288-49
5	185.5	19.3	248	4	US-09-198-603C-2
6	178.5	18.6	161	3	US-09-011-735-6
7	178.5	18.6	351	3	US-09-011-735-1
8	178.5	18.6	351	4	US-09-029-156-1
9	177	18.4	912	5	PCT-US95-03747-2
10	166	17.3	287	1	US-08-365-103B-4
11	166	17.3	300	1	US-08-365-103B-6
12	166	17.3	327	1	US-08-365-103B-2
13	165	17.2	1479	3	US-08-840-062-4
14	160	16.7	1479	3	US-08-840-062-2
15	152	15.8	174	2	US-08-401-530A-5
16	152	15.8	174	2	US-08-709-662-5
17	151	15.7	1487	3	US-08-840-062-7
18	148	15.4	125	5	US-08-722-126A-7
19	148	15.4	125	5	PCT-US95-04258-7
20	148	15.4	166	2	US-08-729-103-4
21	148	15.4	2409	6	US-08-729-103-4
22	142	14.8	108	6	5514582-16
23	140.5	14.6	187	4	US-09-535-521-17
24	140.5	14.6	208	4	US-09-535-521-20
25	140.5	14.6	292	4	US-09-535-521-2
26	140.5	14.6	292	4	US-09-535-521-5
27	138.5	14.4	107	6	5514582-17

28	138	14.4	1455	3	US-08-840-062-5	Sequence 5, Appli
29	137.5	14.3	175	2	US-08-464-637-2	Sequence 2, Appli
30	137.5	14.3	175	2	US-08-401-530A-4	Sequence 4, Appli
31	137.5	14.3	175	2	US-08-709-662-4	Sequence 4, Appli
32	137.5	14.3	175	2	US-08-822-261-3	Sequence 3, Appli
33	136.5	14.2	174	2	US-08-401-530A-6	Sequence 6, Appli
34	136.5	14.2	174	2	US-08-709-662-6	Sequence 6, Appli
35	135	14.1	165	2	US-08-401-530A-7	Sequence 7, Appli
36	135	14.1	165	2	US-08-729-103-3	Sequence 3, Appli
37	135	14.1	165	2	US-08-709-662-7	Sequence 7, Appli
38	134	14.0	128	4	US-09-535-521-8	Sequence 8, Appli
39	134	14.0	139	4	US-09-535-521-11	Sequence 11, Appli
40	134	14.0	141	4	US-09-535-521-14	Sequence 14, Appli
41	131.5	13.7	123	4	US-09-535-521-25	Sequence 25, Appli
42	131.5	13.7	174	1	US-07-778-156-7	Sequence 7, Appli
43	131.5	13.7	174	2	US-08-822-261-4	Sequence 4, Appli
44	131.5	13.7	174	2	US-08-422-166-7	Sequence 7, Appli
45	131.5	13.7	316	4	US-09-111-470-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-469-486-56
; Sequence 56, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoesersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-56
Query Match 100.0%; Score 960; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.4e-102;

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Matches 181: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPPTQPKKIVNAKDVVNTKMFEEELKSRDLTLAQEVALLKEQALQTVCLGKTKVHKMC 60
Db 22 EPPTQPKKIVNAKDVVNTKMFEEELKSRDLTLAQEVALLKEQALQTVCLGKTKVHKMC 81
QY 61 FLAFTQTKTFHEASEDCISRGGLTSTPQTGSENDALYELRQSVGNEAEIWLGLNDMAAE 120
Db 82 FLAFTQTKTFHEASEDCISRGGLTSTPQTGSENDALYELRQSVGNEAEIWLGLNDMAAE 141
QY 121 GTWVDMTGARIYKNNWETETITAPDGGKTENCNCAVLGSAANGKWFDRKRCRDQLPYICQFGI 180
Db 142 GTWVDMTGARIYKNNWETETITAPDGGKTENCNCAVLGSAANGKWFDRKRCRDQLPYICQFGI 201
QY 181 V 181
Db 202 V 202

RESULT 2
US-08-469-658-56
; Sequence 56, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-658-56

Query Match
Best Local Similarity 100.0%; Score 960; DB 2; Length 202;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 22 EPPTQPKKIVNAKDVVNTKMFEEELKSRDLTLAQEVALLKEQALQTVCLGKTKVHKMC 81
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Db 82 FLAFTQTKTFHEASEDCISRGGLTSTPQTGSENDALYELRQSVGNEAEIWLGLNDMAAE 141
QY 121 GTWVDMTGARIYKNNWETETITAPDGGKTENCNCAVLGSAANGKWFDRKRCRDQLPYICQFGI 180
Db 142 GTWVDMTGARIYKNNWETETITAPDGGKTENCNCAVLGSAANGKWFDRKRCRDQLPYICQFGI 201
QY 181 V 181
Db 202 V 202

RESULT 3
US-09-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446CS
; CURRENT APPLICATION NUMBER: US/09/602.877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99

Query Match
Best Local Similarity 44.0%; Score 422.5; DB 4; Length 197;
Matches 80; Conservative 27; Mismatches 46; Indels 3; Gaps 1;
QY 25 ELKSRDLTLAQEVALLKEQALQTVCLGKTKVHKMCFLAFTQTKTFHEASEDCISRGGLT 84
Db 43 DLKQIEKLWTEVNALEIQALQTVCLRGTKVHKKCYLASEGLKHPHEANEDCISKGIL 102
QY 85 STPQTGSENDALYELRQSVGNEAEIWLGLNDMAAEGTWDMTGARIYKNNWETETITAP 144
Db 103 VIPRNSDEINALQDYGRKSLPGVNDLWGLNDMWTEGKFDVNGVNGIAISFLNWD---RAQP 159
QY 145 DGGKTENCNCAVLGSAANGKWFDRKRCRDQLPYICQFGI 180
Db 160 NGKRENCVLFSSQAQKWSDEACRSKRVCFTI 195

RESULT 4
US-08-340-428B-49
; Sequence 49, Application US/08340428B
; Patent No. 5648465
; GENERAL INFORMATION:
; APPLICANT: MARGOLIS, Richard U.
; APPLICANT: RAUCH, Uwe
; APPLICANT: MARGOLIS, Renee K.
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
; TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
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QY	40	LKEQALQTVCLKG-----TKVHM-----KCFLAFTQTKTFHEASEDCISRG	82
Db	663	LEEIEGVRCLLPYGGDLGVLHFCSPGDWAFQACYKHFSARRSWEENKCRMYGA	722
QY	83	TLSTPQTGSNDALYYLRSVGNAEIWLGLNDMAAEGTWDMTGARIAYKNWEITEA	142
Db	723	HLASISTPEODFINNRYETQ-----WIGLNDRTIEGDFLWSDGVPLLYENN--	773
QY	143	QPDGG--KTENCAVLSGAANGKFKRCRDQLPYICQGI	181


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; FILING DATE: 28-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nebel, Heidi S.
; REGISTRATION NUMBER: 37,719
; REFERENCE/DOCKET NUMBER: Uif N5-24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 288-3667
; TELEFAX: (515) 288-1338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-103B-2

Query Match      17.3%  Score 166;  DB 1;  Length 327;
Best Local Similarity 27.2%;  Pred. No. 8.8e-11;
Matches 49;  Conservative 36;  Mismatches 67;  Indels 28;  Gaps 8;

QY 10 IYNAKDVNTWTFELSRDLTAEVALLKEQALQTVCLKGTKVHM-----K 59
Db 143 LVNIKSLGNEK--RTASDSLEKLEQEVAKL---WIELLSKGTACNICPKNLHFQOK 196
QY 60 CFLAETQTKTFHEASEDCISRGTLSTPQTGSENDALYELRQSVGNAEIWLGLNDMAA 119
Db 197 CYFGKGKOWIQARFACSDIQGRVLVSIHSQKEDFLMQHI-----NKKDSWIGLQDLNM 251
QY 120 EGTWDMTGARIAYKNWETEITAQPDGKTKENCVAVLGSAANGKWFDRKCRDQL-PYICQ 177
Db 252 EGEFVWSDGSPGVSNWN---PGEPNNGGQGEDCVMRG--SGQWDAFCRSYLDWVCE 306
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RESULT 13
US-08-840-062-4
; Sequence 4, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/840,062
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-840-062-4
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Query Match      17.2%  Score 165;  DB 3;  Length 1479;
Best Local Similarity 30.7%;  Pred. No. 1.2e-09;
Matches 35;  Conservative 20;  Mismatches 53;  Indels 6;  Gaps 2;

QY 64 FTQKTFHEASEDCISRGTLSTPQTGSENDALYELRQSVGNAEIWLGLNDMAAEGTW 123
Db 253 FQSTLSWREAWASCEQOGADLLSITEHQYINGLL---TGYSSTLWIGLNDLDTSGGW 309
QY 124 VDMTGARIAYKNWETEITAQPDGKTKENCVAVLGSAANGKWFDRKCRDQLPYICQ 177
Db 310 QWSDNSPLKYLNWESD---OPDNPSENCGVIRTESSGGWQNRDCSIALPYVCK 360

RESULT 14
US-08-840-062-2
; Sequence 2, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/840,062
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-840-062-2
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Query Match      16.7%  Score 160;  DB 3;  Length 1479;
Best Local Similarity 30.7%;  Pred. No. 4.3e-09;
Matches 35;  Conservative 19;  Mismatches 54;  Indels 6;  Gaps 2;

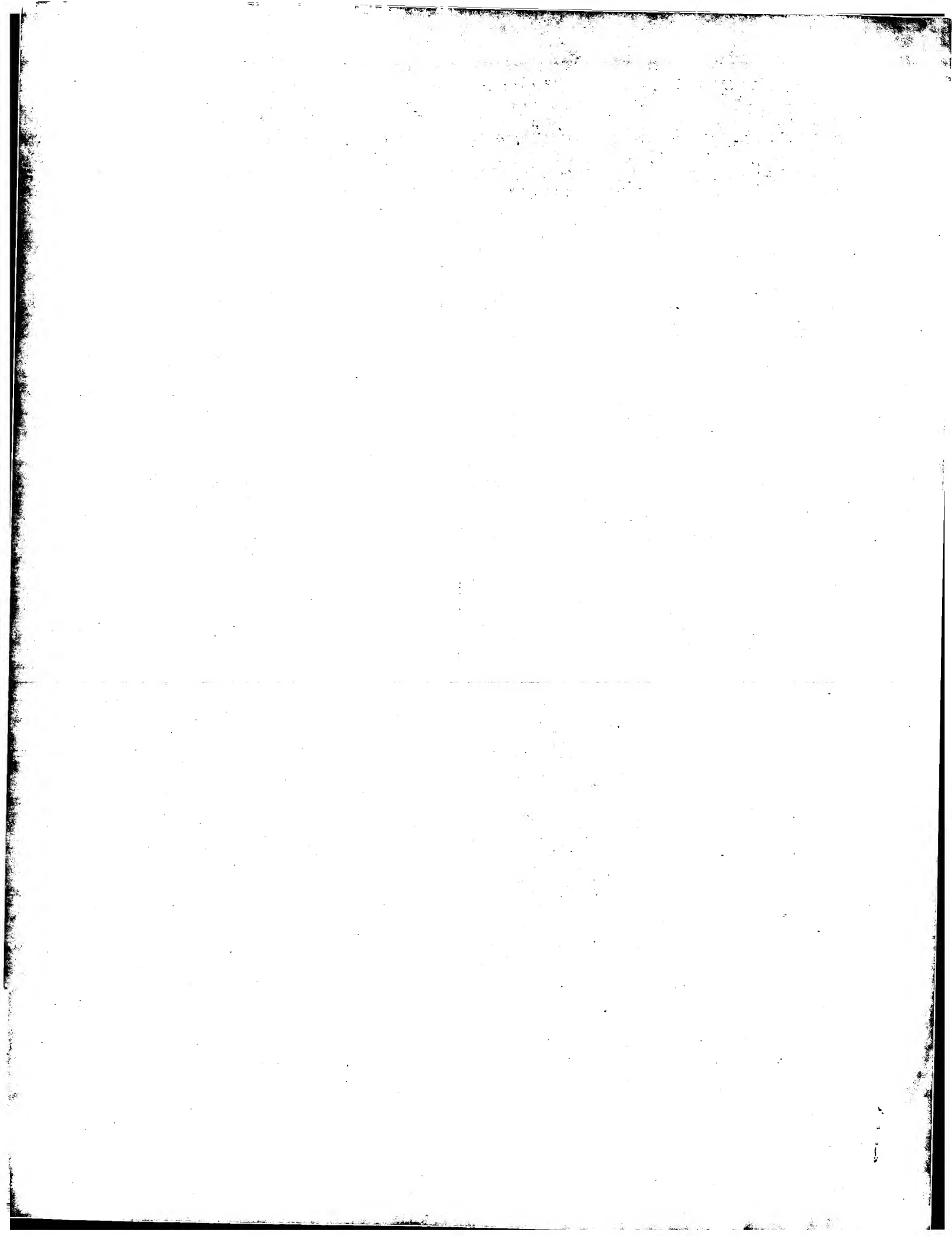
QY 64 FTQKTFHEASEDCISRGTLSTPQTGSENDALYELRQSVGNAEIWLGLNDMAAEGTW 123
Db 252 FQSTLSWREAWASCEQOGADLLSITEHQYINGLL---TGYSSTLWIGLNDLDTSGGW 308
QY 124 VDMTGARIAYKNWETEITAQPDGKTKENCVAVLGSAANGKWFDRKCRDQLPYICQ 177
Db 309 QWSDNSPLKYLNWESD---OPDNPGEENCGVIRTESSGGWQNRDCSIALPYVCK 359

RESULT 15
US-08-401-530A-5
; Sequence 5, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
```

APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-401-530A-5

Query Match 15.8%; Score 152; DB 2; Length 174;
Best Local Similarity 26.7%; Pred. No. 1.4e-09;
Matches 47; Conservative 32; Mismatches 75; Indels 22; Gaps 7;
QY 17 VVNTKMFEEELKRLDTLQAQVALLKEQALQTV-----CLKGTKVH-MKCFIAFTOTKT 69
Db 5 VALTTHSWMLLSLMLLSQ-----VQGEDAKEDVPTSRISCPKGSRAYSGCYALFSVSKS 60
QY 70 FHEASEDCISR-GGTLSTPQTGSNDALYEYLRQSVGNEAEIWLGLNDMAA-----EGTW 123
Db 61 WFDADLACQKRPFGHLVSVLGSSEASFVSLIKSSGNSQNWIGLHDPDTLGOEPNRGCW 120
QY 124 VDMTGARIAYKNWEITEITAPQDGGKTENCACVLSGAANG-KWFDKRCRDOLPYICQF 178
Db 121 EWSNADVMNYFNWET-----NPSSVSGSHGCTLTRASGFLRWRENNCISELPYVCKF 172

Search completed: April 15, 2003, 11:45:56
Job time : 16 secs



GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:43:14 ; Search time 28.75 Seconds
(without alignments)
166.853 Million cell updates/sec

Title: US-09-445-576A-38

Perfect score: 183

Sequence: 1 RRVKEDGDLKTOVEKLREVNALKEMQALQTVCLR 36

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	90.7	197	21	AA828526
2	166	90.7	197	23	AA828526
3	166	90.7	206	21	AAU66756
4	166	90.7	206	22	AAU29161
5	166	90.7	206	22	AAU65279
6	166	90.7	206	23	AAE20465
7	79	43.2	180	20	AAW94264
8	79	43.2	181	20	AAW94256
9	79	43.2	197	20	AAW94262
10	79	43.2	202	15	AAW60521

11	79	43.2	202	22	AAW24034	Human EST encoded
12	79	43.2	228	20	AAW94261	CIH6FTXN123 fusio
13	74	40.4	182	7	AA60098	Sequence of chain
14	69	37.7	52	20	AAW94254	Tetranectin polype
15	69	37.7	73	20	AAW94270	H6FXtripa fusion p
16	64	35.0	49	20	AAW94255	Tetranectin polype
17	64	35.0	65	20	AAW94263	H6FTXN12 fusion pr
18	62	33.9	84	19	AAW43026	Artificial recogni
19	60	32.8	69	20	AAW94271	H6FXtripb fusion p
20	60	32.8	145	20	AAW94266	H6FXtripB-UB fusio
21	60	32.8	330	20	AAW94267	H6FXscFv(CEA6)trip
22	60	32.8	331	20	AAW94268	H6FXtripBscFv(CEA6
23	60	32.8	592	20	AAW94269	H6FXscFv(CEA6)trip
24	59	32.2	84	19	AAW43027	Artificial recogni
25	58	31.7	84	19	AAW43025	Artificial recogni
26	58	31.7	570	22	ABG05601	Novel human diagno
27	57.5	31.4	239	22	AAW95450	Human protein sequ
28	57.5	31.4	369	22	AAW66728	Human muscle BOP p
29	57.5	31.4	428	21	AAW21007	Human nucleic acid
30	57.5	31.4	428	22	AAW39404	Human polypeptide
31	57.5	31.4	501	22	AAW41190	Human polypeptide
32	57	31.1	807	22	AAW95580	Human protein sequ
33	57	31.1	1242	21	AAW53371	Human colon cancer
34	57	31.1	1561	23	ABW97437	Novel human protei
35	55	30.1	11	23	AAU99152	Bovine C-type lect
36	54.5	29.8	442	19	AAW98274	H. pylori GPO 675
37	54.5	29.8	555	22	AAW93869	Human polypeptide,
38	54	29.5	84	19	AAW43028	Artificial recogni
39	53.5	29.2	69	22	AAU22448	Human cardiovascular
40	53.5	29.2	463	22	ABG29607	Novel human diagno
41	53	29.0	81	22	ABW39769	Peptide #7275 enco
42	53	29.0	81	22	AAW60490	Human brain expres
43	53	29.0	81	22	AAW73137	Human bone marrow
44	53	29.0	81	22	AAW33352	Peptide #7389 enco
45	53	29.0	81	23	ABG42985	Human peptide enco

ALIGNMENTS

RESULT 1
AAB28526
ID AAB28526 standard; Protein; 197 AA.
XX
AC AAB28526;
XX
DT 07-FEB-2001 (first entry)
XX
DE Protein encoded by human breast tumour cDNA clone B532S.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy;
KW breast cancer; vaccine.
XX
OS Homo sapiens.
XX
PN WO2000061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US09688.
XX
PR 09-APR-1999; 99US-0288950.
PR 02-JUL-1999; 99US-0346327.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Xu J, Dillon DC;
XX
XX WPI; 2000-638568/61.
XX
XX N-PSDB; AAC79471.
XX
XX A novel isolated polypeptide comprising an immunogenic portion of a
XX breast cancer protein useful in the detection and treatment of breast
PT

polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention.


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PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 18-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090354.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.

PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
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PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
DR N-PSDB; AA265102.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX
PS claim 12; Fig 288; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 206 AA;

Query Match 90.7%; Score 166; DB 21; Length 206;
Best Local Similarity 86.1%; Pred. No. 6.1e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKXKDGDLTKTOVEKLRVFNALKEMQALQTVCLR 36
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Db 44 RRVKXKDGDLTKTOVEKLRVFNALKEMQALQTVCLR 79

RESULT 4
AAU29161
ID AAU29161 standard; Protein; 206 AA.
XX
XX AAU29161;
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XX 18-DEC-2001 (first entry)
DT
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DE Human PRO polypeptide sequence #138.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
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dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 Homo sapiens.

WO200168848-A2.

20-SEP-2001.

28-FEB-2001; 2001WO-US06520.

01-MAR-2000; 2000WO-US05601.

02-MAR-2000; 2000WO-US05841.

03-MAR-2000; 2000US-187202P.

06-MAR-2000; 2000US-186968P.

14-MAR-2000; 2000US-189320P.

14-MAR-2000; 2000US-189328P.

15-MAR-2000; 2000WO-US06884.

21-MAR-2000; 2000US-190828P.

21-MAR-2000; 2000US-191007P.

21-MAR-2000; 2000US-191048P.

26-MAR-2000; 2000US-191314P.

29-MAR-2000; 2000US-192655P.

29-MAR-2000; 2000US-193032P.

30-MAR-2000; 2000US-193053P.

04-APR-2000; 2000WO-US08439.

04-APR-2000; 2000US-194449P.

04-APR-2000; 2000US-194647P.

11-APR-2000; 2000US-195975P.

11-APR-2000; 2000US-196000P.

11-APR-2000; 2000US-196187P.

11-APR-2000; 2000US-196690P.

18-APR-2000; 2000US-196820P.

18-APR-2000; 2000US-198121P.

18-APR-2000; 2000US-198585P.

25-APR-2000; 2000US-199397P.

25-APR-2000; 2000US-199550P.

25-APR-2000; 2000US-199654P.

03-MAY-2000; 2000US-201516P.

17-MAY-2000; 2000WO-US13705.

27-MAY-2000; 2000WO-US14042.

30-MAY-2000; 2000WO-US14941.

02-JUN-2000; 2000WO-US15264.

05-JUN-2000; 2000US-209832P.

28-JUL-2000; 2000WO-US20710.

22-AUG-2000; 2000US-0644848.

04-AUG-2000; 2000WO-US23328.

08-NOV-2000; 2000WO-US30952.

01-DEC-2000; 2000WO-US32678.

20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI: 2001-602746/68.

N-PSDB; AAS46062.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the

presence of tumours, such as prostate and breast tumours, in mammals and

to screen for modulators of the compounds -

Claim 11; Fig 276; 774pp; English.

Sequences AAU29324-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to

detect the presence of a tumour in a mammal by comparing the level of

expression of a PRO polypeptide in a test sample of cells from the animal

and a control sample of normal cells, whereby a higher level of

expression in the test sample indicates the presence of a tumour in the

mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats

CC and rabbits but are preferably human. The polypeptides can be used to

stimulate tumour necrosis factor (TNF) alpha release from human blood.

when contacted with it. A specific polypeptide can be used to stimulate

the proliferation or differentiation of chondrocyte cells. The PRO

proteins can be used to determine the presence of tumours and also

susceptibility to tumour development, particularly adrenal, lung, colon,

breast, prostate, rectal, cervical, or liver tumours, in mammalian

subjects. The oligonucleotide probes specific for the PRO nucleic acids

can be used for genetic analysis of individuals with genetic disorders.

XX Sequence 206 AA:

Query Match

Best Local Similarity 90.7%; Score 166; DB 22; Length 206;

Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRVKEKDGDLTKQVEKLWREVNALKEMQALQTVCLR 36

Db 44 RRVKDKGDLTKQIEKLWTEVNALKEMQALQTVCLR 79

RESULT 5

AAB65279

ID AAB65279 standard; Protein; 206 AA.

AC AAB65279;

XX 02-APR-2001 (first entry)

Human PRO1345 (UNQ700) protein sequence SEQ ID NO:403.

Human; secreted and transmembrane protein; PRO; cytostatic;

cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

diagnostic assay.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 17-AUG-1999; 99US-0149396.

XX 15-SEP-1999; 99WO-US21090.

XX 08-OCT-1999; 99US-0158663.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44248.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 288; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 206 AA;
 Query Match 90.7%; Score 166; DB 22; Length 206;
 Best Local Similarity 86.1%; Pred. No. 6.1e-14;
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RRVKEDGDLKTQVEKLMREVNALKEQALQTVCLR 36
 DB 44 RRVKEDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79
 RESULT 6
 AAE20465
 ID AAE20465 standard; Protein; 206 AA.
 XX
 AC AAE20465;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human tumour-associated antigenic target-173 (TAT173) protein.
 XX
 KW Human; tumour-associated antigenic target-173; TAT173; cytostatic;
 KW gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1..31
 FT /label= Signal_peptide
 FT Protein 32..206
 FT /label= Mature_TAT173_protein
 FT Modified-site 14..20
 FT /label= N-myristoylation_site
 FT Modified-site 126..130
 FT /label= Amidation_site
 FT Modified-site 155..161
 FT /label= N-myristoylation_site
 FT Modified-site 170..174
 FT /label= Amidation_site
 FT Domain 176..201
 FT /note= "C-type lectin domain signature"
 XX
 PN WO200216602-A2.
 XX
 PD 28-FEB-2002.

XX 23-AUG-2001; 2001WO-US26626.
 XX
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US26678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Polakis P;
 PI Williams PM, Wood WI, Wu TD, Zhang Z;
 XX
 DR WPI: 2002-292065/33.
 DR N-PSDB; AAD32720.
 XX
 CC New antibodies that bind tumor-associated antigenic target (TAT)
 CC polypeptides, useful for treating and diagnosing tumor (e.g. breast,
 CC lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle,
 CC pigs, goats, rabbits or humans -
 XX
 PS Claim 1; Fig 10; 124pp; English.
 XX
 CC The present invention relates to an isolated antibody that binds to
 CC tumor-associated antigenic target (TAT) polypeptide. The antibody is
 CC used for treating and diagnosing tumours (e.g. breast, lung, liver or
 CC stomach tumours) in mammals, e.g. dogs, cats, cattle, horses, sheep,
 CC pigs, goats, rabbits, or preferably humans. The antibody may also be
 CC used in antibody-dependent enzyme mediated prodrug therapy (ADEPT).
 CC The antibody is also useful for the therapeutic treatment or for the
 CC diagnostic detection of cancer. TAT cDNA is useful in gene therapy.
 CC The present sequence is human TAT173 protein. TAT173 cDNA is designated
 CC as DNA64852-1589.
 XX
 SQ Sequence 206 AA;
 Query Match 90.7%; Score 166; DB 23; Length 206;
 Best Local Similarity 86.1%; Pred. No. 6.1e-14;
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RRVKEDGDLKTQVEKLMREVNALKEQALQTVCLR 36
 DB 44 RRVKEDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79
 RESULT 7
 AAW94264
 ID AAW94264 standard; protein; 180 AA.
 XX
 AC AAW94264;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE H6EXTN23 fusion protein sequence.
 XX
 KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; H6EXTN23.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9856906-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-DK00245.
 XX
 PR 11-JUN-1997; 97DK-0000685.

XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI; 1999-080897/07.
 DR
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Disclosure; Fig 8: 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXTN23 fusion protein sequence. The specification claims
 CC that the heterologous moiety to which the TTSEs of the invention are
 CC linked to is specifically different from the present fusion protein
 CC sequence.
 XX
 SQ Sequence 180 AA;
 Query Match 43.2%; Score 79; DB 20; Length 180;
 Best Local Similarity 57.1%; Pred. No. 0.014;
 Matches 16; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Qy 9 DLKTOVEKWLREYNALKEMQALQTVCLR 36
 Db 24 ELKSRDLTLAQEVALLEKQALQTVCLK 51
 RESULT 8
 AAW94256
 ID AAW94256 standard; protein; 181 AA.
 AC AAW94256;
 AC AAW94256;
 DT 26-APR-1999 (first entry)
 XX Human tetranectin amino acid sequence.
 DE
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.
 XX

OS Homo sapiens.
 XX
 PN W09856906-A1.
 XX
 PD 17-DEC-1998.
 XX
 XX 11-JUN-1998; 98WO-DK00245.
 PF
 XX 11-JUN-1997; 97DK-0000685.
 PR
 XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI; 1999-080897/07.
 DR
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Claim 10; Page 60; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a human tetranectin sequence from which the TTSE can be
 CC derived.
 XX
 SQ Sequence 181 AA;
 Query Match 43.2%; Score 79; DB 20; Length 181;
 Best Local Similarity 57.1%; Pred. No. 0.014;
 Matches 16; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Qy 9 DLKTOVEKWLREYNALKEMQALQTVCLR 36
 Db 25 ELKSRDLTLAQEVALLEKQALQTVCLK 52
 RESULT 9
 AAW94262
 ID AAW94262 standard; protein; 197 AA.
 XX
 AC AAW94262;
 AC AAW94262;
 DT 26-APR-1999 (first entry)
 XX

FT Disulfide-bond 77..176
 FT Disulfide-bond 152..168
 FT Misc-difference 37
 FT /label= M,V
 XX
 XX EP206400-A.
 XX
 XX 30-DEC-1986.
 XX
 XX 10-JUN-1986; 86EP-0201005.
 XX
 XX 11-JUN-1985; 85NL-0001682.
 XX
 XX (NEDE) NEDERLAND ORG TNO.
 XX
 XX Duhl Clemmensen I, Klufft C;
 XX
 XX WPI; 1986-340760/52.
 XX
 XX New Tetranectin protein - purified from human blood plasma by
 PT e.g. affinity chromatography on a column with coupled kringle 4
 PT of plasminogen
 XX
 XX Claim 9; Page 1a; 12pp; English.
 XX
 XX Tetranectin is comprised of four polypeptide chains having the
 CC formula shown in AAP60098. Tetranectin stimulates and controls the
 CC plasminogen activation resulting in a higher rate of clot lysis or
 CC fibrinolysis, esp. in the presence of blood platelets and in the
 CC presence of a complex fibrin clot from blood. It stimulates and
 CC controls the plasminogen activation in the absence of fibrin but in
 CC the presence of a cofactor such as polylysine.
 XX
 XX Sequence 182 AA;
 SQ
 Query Match 40.4%; Score 74; DB 7; Length 182;
 Best Local Similarity 53.6%; Pred. No. 0.065;
 Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 9 DLKTQVEKLMREYNALKEMOALQTVCLR 36
 :||:::|:| ||| ||||| |
 Db 25 ELKSRLDTLAQEXALLKEQOALQTVCLK 52
 RESULT 14
 AAW94254
 ID AAW94254 standard; Protein; 52 AA.
 XX
 XX AC AAW94254;
 XX
 XX 26-APR-1999 (first entry)
 XX
 XX Tetranectin polypeptide fragment (residues 1-52).
 DE
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 XX fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.
 XX
 XX Homo sapiens.
 XX
 XX W09856906-A1.
 XX
 XX 17-DEC-1998.
 XX
 XX 11-JUN-1998; 98WO-DK00245.
 XX
 XX 11-JUN-1997; 97DK-0000685.
 XX
 XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.

XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thøgersen HC;
 XX
 XX WPI; 1999-080897/07.
 DR
 XX
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 XX Example 1; Page 59; 110pp; English.
 PS
 XX
 XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a human tetranectin polypeptide fragment. The encoding nucleic
 CC acid sequence was amplified by PCR from the plasmid clone pT7H6FXTN123.
 CC This is used in the construction of E. coli expression vectors for the
 CC production of trimerised chimeric fusion proteins.
 XX
 XX Sequence 52 AA;
 SQ
 Query Match 37.7%; Score 69; DB 20; Length 52;
 Best Local Similarity 53.6%; Pred. No. 0.071;
 Matches 15; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 9 DLKTQVEKLMREYNALKEMOALQTVCLR 36
 :||:::|:| ||| ||||| |
 Db 25 ELKSRLDTLAQEXALLKEQOALQTVSLK 52
 RESULT 15
 AAW94270
 ID AAW94270 standard; protein; 73 AA.
 XX
 XX AC AAW94270;
 XX
 XX 26-APR-1999 (first entry)
 XX
 XX H6FXTripa fusion protein sequence.
 DE
 XX
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX W09856906-A1.
 PN
 XX

Search completed: April 15, 2003, 11:47:59
Job time : 29.75 secs

GenCore version 5.1.4_p5_4578
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OW protein - protein search, using sw model

Run on: April 15, 2003, 11:44:50 ; Search time 22.5 Seconds
(without alignments)
329.675 Million cell updates/sec

Title: US-09-445-576A-37
Perfect score: 171
Sequence: 1 LVSSKMFELKRNMDVLAQEVALLKEKQALQTVCLK 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	71.3	201	13 Q9DDDD4	Q9dd44 gallus gall
2	79	46.2	196	11 Q9EPW4	Q9epw4 mus musculu
3	76	44.4	197	6 Q28008	Q28008 bos taurus
4	61	35.7	1212	5 Q9XZ29	Q9xz29 drosophila
5	60.5	35.4	512	2 Q84930	Q84930 trichodesmi
6	58	33.9	185	16 Q8R8C6	Q8r8c6 thermosae
7	57	33.3	654	17 Q8TT21	Q8tt21 methanosar
8	57	33.3	920	16 Q9A0U7	Q9a0u7 streptococc
9	56.5	33.0	83	10 Q8S9M9	Q8s9m9 oryza sativ
10	56.5	33.0	323	10 Q43529	Q43529 lycopersico
11	56	32.7	710	4 Q9C0B2	Q9c0b2 homo sapien
12	55.5	32.5	1970	10 Q9LM53	Q9lm53 arabidopsis
13	55	32.2	857	2 Q69287	Q69287 campylobact
14	55	32.2	857	16 Q9PI02	Q9pi02 campylobact
15	54.5	31.9	634	10 Q9MAA6	Q9maa6 arabidopsis
16	54.5	31.9	1833	5 Q9VM67	Q9vm67 drosophila

17	54	31.6	739	5 Q9VJP8	Q9vjp8 drosophila
18	54	31.6	751	5 Q9NKG2	Q9nk92 drosophila
19	54	31.6	761	4 Q14689	Q14689 homo sapien
20	54	31.6	1549	5 Q20060	Q20060 caenorhabdi
21	54	31.6	1609	5 Q9GRC3	Q9grc3 caenorhabdi
22	54	31.6	1893	5 Q17887	Q17887 caenorhabdi
23	54	31.6	1978	4 Q15154	Q15154 homo sapien
24	54	31.6	2759	5 Q45614	Q45614 caenorhabdi
25	54	31.6	3102	5 Q9TZR4	Q9tzt4 caenorhabdi
26	53.5	31.3	1014	5 Q26152	Q26152 plasmodium
27	53.5	31.3	1915	12 Q8U1V9	Q8uyv9 strawberry
28	53	31.0	794	17 Q8ZVH4	Q8zvh4 pyrobaculum
29	53	31.0	895	4 Q9U147	Q9ui47 homo sapien
30	53	31.0	908	16 Q929F2	Q929f2 listeria in
31	53	31.0	1660	10 Q9S1R1	Q9s1rl arabidopsis
32	53	31.0	1979	4 Q95949	Q95949 homo sapien
33	52.5	30.7	486	10 Q9M3Z2	Q9m3z2 cicor ariet
34	52	30.4	84	16 Q92RQ4	Q92rq4 rhizobium m
35	52	30.4	168	10 Q96433	Q96433 glycine max
36	52	30.4	170	10 Q8W2E2	Q8w2e2 glycine max
37	52	30.4	170	10 Q8W2E1	Q8w2e1 glycine max
38	52	30.4	213	16 Q9K9R4	Q9k9r4 bacillus ha
39	52	30.4	486	10 Q22909	Q22909 arabidopsis
40	52	30.4	609	16 Q8Y1Z9	Q8yi29 brucella me
41	52	30.4	956	10 Q9C7B9	Q9c7b9 arabidopsis
42	52	30.4	967	5 Q9NGX2	Q9ngx2 entamoeba h
43	52	30.4	1033	10 Q9LHL9	Q9lhl9 arabidopsis
44	52	30.4	1096	5 Q9NGX1	Q9ngx1 entamoeba h
45	52	30.4	1410	5 Q97230	Q97230 plasmodium

ALIGNMENTS

RESULT 1

-----Q9DDDD4-----
ID Q9DDDD4 PRELIMINARY; PRT; 201 AA.
AC Q9DDDD4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tetranectin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Wewer U.M.;
RT "tetranectin in chicken."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277116; CAC20217.1; -.
DR HSSP; P05452; 1TN3.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;

Query Match 71.3%; Score 122; DB 13; Length 201;
Best Local Similarity 74.3%; Pred No. 1.8e-07;
Matches 26; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 VSSKMFELKRNMDVLAQEVALLKEKQALQTVCLK 36
||| ||| :|:|||||||
Db 38 VSLKMIEDLKAMIDNISQEVALLKEKQALQTVCLK 72

RESULT 2

Q9EPW4 PRELIMINARY; PRT; 196 AA.
ID Q9EPW4

```

AC Q9EPW4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C-type lectin superfamily 1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES129/SV.
RA Neame P.J., Grimm D.R.;
RT "Mouse homolog of human CLEC5F1, a cartilage derived C-type lectin.";
BL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF317204; AAG48620.1; -.
DR HSSP; P05452; 1HTN.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C.1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ
Query Match 46.2%; Score 79; DB 11; Length 196;
Best Local Similarity 55.2%; Pred. No. 0.036;
Matches 16; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Qy 8 EELKNDVLAQEVALLKEKQALQTVCLK 36
Db 42 DLLASQVEKLWREVNALKEMQALQTVCLR 70

RESULT 3
Q28008 PRELIMINARY; PRT; 197 AA.
AC Q28008;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE C-type lectin homolog precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARTILAGE;
RA Neame P.J., Boynton R.E.;
RT "C-type lectin homolog from bovine cartilage.";
BL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22298; AAC18614.1; -.
DR HSSP; P05452; 1TN3.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 197 C-TYPE LECTIN HOMOLOG.
SQ SEQUENCE 197 AA; 22215 MW; 22215 MW; AACAC280F41AC0F4 CRC64;

Query Match 44.4%; Score 76; DB 6; Length 197;
Best Local Similarity 57.1%; Pred. No. 0.086;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Qy 9 ELKNDVLAQEVALLKEKQALQTVCLK 36
Db 43 DLKQVEKLWREVNALKEMQALQTVCLR 70

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RESULT 4
Q9XZ29 PRELIMINARY; PRT; 1212 AA.
ID Q9XZ29;
AC Q9XZ29;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE KLP3A protein.
GN KLP3A OR BGDNA:LD21815 OR EG:BACR25B3.9 OR CG8590.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Karpis D.M., Nelson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Murphy L., Harris D., Barrell B.;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Benos P.;
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbayani A., Arcalena T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacle J.M.,

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	Park S., Sequeira A., Sethi H., Snir E., Swirskas R.R., Weinburg T.,
RA	Celniker S.E.;
RL	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AE003424; AAF45793.1; -;
DR	EMBL; ALI38972; CAB72294.1; -;
DR	EMBL; AF132186; AAD34774.1; -;
DR	HSSP; PF17119; 3KAR
DR	FlyBase; FBgn0011606; klp3A.
DR	InterPro; IPR001752; kinesin_motor.
DR	Pfam; PFO02225; kinesin; 1.
DR	PRINTS; PRO0380; KINESINHEAVY.
DR	SMART; SMU0129; KISC; 1.
DR	PROSITE; PS00411; KINSIN_MOTOR_DOMAIN1; UNKNOWN_1.
DR	PROSITE; PSS0067; KINSIN_MOTOR_DOMAIN2; 1.
KW	Atp-binding; Coiled coil; Hypothetical protein; Microtubules; Motor protein.
SQ	SEQUENCE 1212 AA; 135811 MW; 7ADAD60AG9B1CC4E CRC64;
	Query Match 35.7%; Score 61; DB 5; Length 1212;
	Best Local Similarity 37.1%; Pred. No. 35;
Matches	13; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY	2 VSKMFEELKNRMDVLAQEVALLEKEQAQTVCCLK 36 : : : : : : : :: : : :
Dd	609 ISAKLAERKRQLLEEQETSDLRKKLTQNALLK 643
	RESULT 5
O84930	PRELIMINARY; PRT; 512 AA.
ID O84930	
AC O84930	
DT 01-NOV-1998	(TEMBLrel. 08, Created)
DT 01-JUN-1998	(TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002	(TEmBLrel. 21, Last annotation update)
DE MOF	E protein of nitrogenase beta subunit (EC 1.18.6.1) (NIFK).
GN NIFK	
OS Trichodesmium sp. (strain IMS101).	
OC Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium.	
OX NCBI_TaxID=57878;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=IMS101;	
RD Dominic B., Zehr J.P.:	
RT "Cloning, sequencing and transcriptional analysis of contiguous nifHDK	
RT operon reveals unexpected nifD, nifDK and nifK transcripts in	
RT Trichodesmium sp. IMS101."	
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. [2]	
RP SEQUENCE FROM N.A.	
RD Dominic B., Zani S., Chen Y.-B., Mellon M.T., Zehr J.P.;	
RT "Organization of the nif genes of the nonheterocystous cyanobacterium	
RT Trichodesmium sp. IMS101;"	
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.	
DR EMBL; AF016484; AAD03798.1; -;	
DR EMBL; AF167538; AAF82639.1; -;	
DR HSP; P07329; 3MIN.	
DR InterPro; IPR000318; Nitrogense_comp1.	
DR InterPro; IPR000510; Oxred_nitrognse1.	
DR Pfam; PFO0148; oxidored_nitro; 1.	
DR TGFRAMS; TTGR01286; nifk; 1.	
DR PROSITE; PS006699; NITROGENASE_1_1; 1.	
DR DR PROSITE; PS00090; NITROGENASE_1_2; 1.	
KW Oxidoreductase.	
SQ SEQUENCE 512 AA; 56936 MW; 81E4D27A75ABAEDF CRC64;	
	Query Match 35.4%; Score 60.5; DB 2; Length 512;
	Best Local Similarity 46.3%; Pred. No. 18;
Matches	19; Conservative 3; Mismatches 12; Indels 7; Gaps 2;
QY	2 VSKMFEE-----LKRMVDVLAQEVALLEKEQO-ALOTVCVL 35 : : : : : : : : : :
Dd	113 VSSMTEDA AVFGCKNM DGLANSYA LYPKRKIALCTTCM 153

Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 SKMFEELKRMVDVLAQEVALLKEQ 28
I : I I I I I : I I I I I : I
Db 255 SLLFRELKHREALRQETIFLKDDQ 279

RESULT 8

Q9A007 PRELIMINARY; PRT: 920 AA.

ID Q9A007
AC Q9A007;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
GN PC OR SPY0608.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; Pubmed=11296296;
RA Ferretti J.-J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., McLaughlin R.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
RT "complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC -!- SOURCE FOR THE TRICARBOXYLIC ACID CYCLE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ORTHOPHOSPHATE + OXALOACETATE = H(2)O +
CC -!- PHOSPHOENOLPYRUVATE + CO(2).
CC -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
DR EMBL; AE006516; AAK33584.1; -
DR HSSP; P00864; 1FIY.
DR InterPro; IPR001449; PEPCase.
DR Pfam; PF00311; PEPCase; 1.
DR PRINTS; PR00150; PEPCARBLASE.
DR PROSITE; PS00781; PEPCASE_1; 1.
DR PROSITE; PS00393; PEPCASE_2; 1.
KW Carbon dioxide fixation; Lyase; Pyruvate; Tricarboxylic acid cycle;
KW Complete proteome.
SQ SEQUENCE 920 AA; 104751 MW; 464EAA309A2237 CRC64;

Query Match 33.3%; Score 57; DB 16; Length 920;
Best Local Similarity 61.1%; Pred. No. 84;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 ELKRMVDVLAQEVALLKE 26
I : I I I I I I I I I I
Db 7 ESSNQDIIEEVALKE 24

RESULT 9

Q8S9M9 PRELIMINARY; PRT: 83 AA.

ID Q8S9M9
AC Q8S9M9;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Putative transcription factor (Fragment).
GN OCS1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Quanhong Y., Rihe P., Aisheng X., Xian L., Huiqin F.;

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Query Match          32.58;  Score 55.5;  DB 10;  Length 1970;
Best local Similarity 38.2%;  Pred. No. 2.7e+02;
Matches 13;  Conservative 8;  Mismatches 10;  Indels 3;  Gaps 1;

QY      2  VSSKMFELKRMVDVLAQAEVALLKEKQALQTVCL 35
      :|:|  |||:|:|  |||:|:|  |||:|:|
Db      776  LSTAEKELKQRLDITLDEVCSLKEE---KTTCI 806

RESULT 13
O69287      PRELIMINARY;          PRT;      857  AA.
AC O69287;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heat shock protein.
GN CLPB.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE=99214069; PubMed=10196475;
RX Thies F.L., Karch H., Hartung H.P., Giegerich G.;
RT "The ClpB protein from Campylobacter jejuni: molecular
RT characterization of the encoding gene and antigenicity of the
RT recombinant protein.";
RL Gene 230:61-67(1999).
DR EMBL; Y13333; CAA73776.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR001270; Chaprnlnc_clpA/B.
DR InterPro; IPR004176; Clp_N.
DR Pfam; PF00004; AAA; 2.
DR Pfam; PF02861; Clp_N; 2.
DR PRINTS; PR00300; CLPPROTEASEA.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00870; CLPAB_1; 1.
DR PROSITE; PS00871; CLPAB_2; 1.
KW ATP-binding.
SQ SEQUENCE      857  AA;  95442  MW;  253A7EFCB3D76487  CRC64;

Query Match          32.28;  Score 55;  DB 2;  Length 857;
Best local Similarity 53.8%;  Pred. No. 1.4e+02;
Matches 14;  Conservative 5;  Mismatches 5;  Indels 2;  Gaps 1;

QY      5  KMFEELKN--RMDVLAQAEVALLKEKQ 28
      ||  :||  |||:|:|  |||:|:|
Db      430  KMENDEKNQKRLDEIAKELANLKEKQ 455

RESULT 14
Q9PI02      PRELIMINARY;          PRT;      857  AA.
AC Q9PI02;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ATP-dependent Clp protease ATP-binding subunit.
GN CLPB OR CJ0509C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RS SEQUENCE FROM N.A.
RA STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

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Search completed: April 15, 2003, 11:50:11
Job time : 24.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:44:09 ; Search time 6.5 Seconds
(without alignments)
229.715 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSSKMFELKRMVDLAQEVALLKEKQALQTFVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	171	100.0	202	1	TETN_MOUSE	P43025	mus musculus
2	146	85.4	202	1	TETN_HUMAN	P05452	homo sapien
3	89	52.0	166	1	TETN_CARSP	P26258	carcharinu
4	72	42.1	197	1	CLFI_HUMAN	O75596	homo sapien
5	55	32.2	224	1	XJD7_YEAST	P47056	saccharomyc
6	55	32.2	524	1	YE33_SYNY3	P74217	synecocyst
7	55	32.2	591	1	VATA_CHLMU	Q9pk85	chlamydia m
8	55	32.2	2179	1	POLG_HRV14	P03303	human rhino
9	54	31.6	1957	1	YD86_SCHPO	Q10411	schizosacch
10	53.5	31.3	402	1	ELAD_ECOLI	Q47013	escherichia
11	53.5	31.3	513	1	NIFK_RHISN	P19067	rhizobium s
12	52	30.4	425	1	SYS_BACHD	Q9kg94	bacillus ha
13	52	30.4	852	1	RA50_THEMEA	Q9xix1	thermotoga
14	52	30.4	1010	1	ALA3_CHICK	P24798	gallus gall
15	51	29.8	359	1	MCAL_CRIGR	O54873	cricketulus
16	51	29.8	513	1	NIFK_BRASP	P06122	bradyrhizob
17	51	29.8	591	1	VATA_CHLTR	O84310	chlamydia t
18	51	29.8	1013	1	ALA3_RAT	P06687	rattus norv
19	50.5	29.5	356	1	NIFK_HERSE	P77875	herbaspiril
20	50.5	29.5	372	1	PARA_HUMAN	Q9nvc7	homo sapien
21	50.5	29.5	372	1	PARA_MOUSE	Q9nvc1	mus musculus
22	50.5	29.5	372	1	PARA_RAT	Q9hb97	rattus norv
23	50.5	29.5	511	1	NIFK_CVAA5	C07643	cyanothece
24	50.5	29.5	4367	1	DYHC_NEUCR	P45443	neurospora
25	50	29.2	110	1	YHBJ_ACTAC	P96769	actinobacil
26	50	29.2	210	1	YADS_AERPU	Q9r9s0	aeromonas p
27	50	29.2	310	1	MCAL_MOUSE	P31230	mus musculus
28	50	29.2	620	1	DNAL_PORPU	P30723	porphyra pu
29	50	29.2	722	1	MEPL_TORAC	Q9m714	nicotiana t
30	49.5	28.9	489	1	PT94_YEAST	P07390	saccharomyc
31	49.5	28.9	518	1	NIFK_THIFE	P15052	thiobacillus
32	49.5	28.9	679	1	YKR9_YEAST	P34237	saccharomyc
33	49.5	28.9	1260	1	MY5B_HUMAN	Q9ulv0	homo sapien

RESULT 1

ID	TETN_MOUSE	STANDARD	PRT	202 AA
AC	P43025			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).			
GN	TNA			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CS7BL/6 X CBA; TISSUE=Lung;			
RX	MEDLINE=95137396; PubMed=7835708;			
RA	Soerensen C.B., Berglund L., Petersen T.E.;			
RT	"Cloning of a cDNA encoding murine tetranectin."			
RL	Gene 152:243-245(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=96116955; PubMed=8563165;			
RA	Ibaraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.;			
RT	"Mouse tetranectin: cDNA sequence, tissue-specific expression, and chromosomal mapping."			
RL	Mamm. Genome 6:693-696(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Liver;			
RX	MEDLINE=98072445; PubMed=9409787;			
RA	Soerensen C.B., Berglund L., Petersen T.E.;			
RT	"Cloning of the murine tetranectin gene and 5'-flanking region."			
RL	Gene 201:199-202(1997).			
CC	-!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle 4. May be involved in the packaging of molecules destined for exocytosis (By similarity).			
CC	-!- SUBUNIT: Homotrimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL MUSCLE.			
CC	-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL; X79199; CAA55791.1; -			
DR	EMBL; U08595; AAA96811.1; -			
DR	EMBL; X98122; CAA66804.1; -			
DR	HSSP; P05452; 1TN3.			

P41129 brassica na
P54482 bacillus su
P35616 xenopus lae
O43303 homo sapien
P58312 oreochromis
Q09222 caenorhabdi
P35900 saccharomyc
P45024 haemophilus
Q38226 methanococc
P39255 bacterioph
P18848 homo sapien
P37464 bacillus su

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DR MGD; MGI:104540; Tna.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
KW PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT LECTIN; Plasma; Signal.
FT SIGNAL 1 21
FT CHAIN 22 202
FT DOMAIN 77 198
FT DISULFID 71 81
FT DISULFID 98 197
FT DISULFID 173 189
FT CONFLICT 19 20
FT CONFLICT 84 84
FT CONFLICT 180 180
FT CONFLICT 188 188
SQ SEQUENCE 202 AA; 22527 MW; 639E7334D58EB04E CRC64;

Query Match 100.0%; Score 171; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 3; le-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVSSKMFELKRMNDVLAQAEVALLKEKQALQTVCLK 36
DB 38 LVSSKMFELKRMNDVLAQAEVALLKEKQALQTVCLK 73
|||||
|||||

RESULT 2
TETN_HUMAN
ID TETN_HUMAN STANDARD; PRT; 202 AA.
AC P03452;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92365345; PubMed=1354271;
RA Wexer U.M., Albrechtsen R.;
RT "Tetranectin, a plasminogen kringle 4-binding protein. Cloning and
RL gene expression pattern in human colon cancer.";
RL Lab. Invest. 67:253-262(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92380263; PubMed=1511740;
RA Berglund L., Petersen T.E.;
RT "The gene structure of tetranectin, a plasminogen binding protein.";
RL FEBS Lett. 309:15-19(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58.
RX MEDLINE=88107595; PubMed=3427041;
RA Fuldendorff J., Clemmensen I., Magnusson S.;
RT "Primary structure of tetranectin, a plasminogen kringle 4 binding
RT plasma protein: homology with asialoglycoprotein receptors and
RT cartilage proteoglycan core protein.";
RL Biochemistry 26:6757-6764(1987).
RN [5]
RP SEQUENCE OF 1-36 FROM N.A.
RC TISSUE=Placenta;
RA Sorensen C.B., Berglund L., Petersen T.E.;
RT "Cloning and mapping of the murine tetranectin gene.";

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RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106.
RC TISSUE=Plasma;
RX MEDLINE=20080486; PubMed=10614823;
RA Jaquinod M., Holtet T.B., Ezerodt M., Clemmensen I., Thøgersen H.C.,
RA Roepstorff P.;
RT "Mass spectrometric characterisation of post-translational
RT modification and genetic variation in human tetranectin.";
RL Biol. Chem. 380:1307-1314(1999).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.8 ÅNGSTRÖMS).
RX MEDLINE=97398360; PubMed=9256258;
RA Nielsen B.B., Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H.,
RA Ezerodt M., Thøgersen H.C., Larsen I.K.;
RT "Crystal structure of tetranectin, a trimeric plasminogen-binding
RT protein with an alpha-helical coiled coil.";
RL FEBS Lett. 412:388-396(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ÅNGSTRÖMS) OF 66-202.
RX MEDLINE=98437604; PubMed=9757090;
RA Kastrup J.S., Nielsen B.B., Rasmussen H., Holtet T.L., Graversen J.H.,
RA Ezerodt M., Thøgersen H.C., Larsen I.K.;
RT "Structure of the C-type lectin carbohydrate recognition domain of
RT human tetranectin.";
RL Acta Crystallogr. D 54:757-766(1998).
CC -1- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules destined for
CC exocytosis.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=20535.8; MW_ERR=2.4; METHOD=Electrospray;
CC RANGE=22-202.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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CC -----
CC EMBL; X70910; CAA50265.1; -
CC EMBL; X70911; CAA50265.1; JOINED.
CC EMBL; X70912; CAA50265.1; JOINED.
CC EMBL; X64559; CAA43860.1; -
CC EMBL; BC011024; AAH11024.1; -
CC EMBL; X98121; CAA66803.1; -
CC PIR; A29747; A29747.
CC PIR; S19865; S19865.
CC PIR; S24126; S24126.
CC PDB; 1HTN; 03-DEC-97.
CC PDB; 1TN3; 06-MAY-98.
CC Genew; HGNC:11891; TNA.
CC MIM; 187520; -
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW LECTIN; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 202
FT DOMAIN 77 198
FT DISULFID 71 81
FT DISULFID 98 197
FT DISULFID 173 189
FT CARBOHYD 25 25
FT VARIANT 55 55
FT VARIANT 58 58
FT VARIANT 58 58
FT /FTid=VAR_004189.
FT /FTid=VAR_004190.

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CC EMBL: Z49312; CAA89328.1; -
DR SGD: S0003574; YJL037W.
FW Hypothetical protein; Transmembrane.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
SQ SEQUENCE 224 AA; 24746 MW; 6C17841176EADClF CRC64;

Query Match 32.2%; Score 55; DB 1; Length 224;
Best Local Similarity 44.4%; Pred. No. 6.7;
Matches 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 VSSKMFELKKNRMDVLAQEVALLKEKQ 28
D 136 VSTRKFESLLNKYDLVAKKGELTEEQ 162

RESULT 6
YE33_SYNY3
ID YE33_SYNY3 STANDARD; PRT; 524 AA.
AC P74217;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein sll1433.
GN SLL1433.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuda A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.,
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0031 FAMILY.
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CC -----
DR EMBL: D90913; BAAL8311.1; -
DR InterPro: IPR000631; UPF0031.
DR InterPro: IPR004443; YJef_wterm.
DR Pfam: PF01256; UPF0031.1.
DR TIGRFAMs: TIGR00196; YJef_cterml; 1.
DR TIGRFAMs: TIGR00197; YJef_nterm; 1.
DR PROSITE: PS01049; UPF0031_1; 1.
DR PROSITE: PS01050; UPF0031_2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 524 AA; 55225 MW; 7E152799D04133D7 CRC64;

Query Match 32.2%; Score 55; DB 1; Length 524;
Best Local Similarity 40.6%; Pred. No. 16;
Matches 13; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 LVSSKMFELKKNRMDVLAQEVALLKEKALQ 32
D 11 VVSAQMGEIENWLFQTGMPVAALMEKALQ 42

RESULT 7

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VATA_CHLMU
ID VATA_CHLMU STANDARD; PRT; 591 AA.
AC Q9PK65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE V-type ATP synthase alpha chain (EC 3.6.3.14) (V-type ATPase subunit
DE A).
GN ATPA OR TC0582.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MoPn / N199;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumonae AR39."
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE V-TYPE ALPHA CHAIN IS A
CC CATALYTIC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC -----
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CC -----
DR EMBL: AE002326; AAF39416.1; -
DR TIGR: TC0582;
DR InterPro: IPR000793; ATPase_a/bc.
DR InterPro: IPR004100; ATPase_a/bn.
DR InterPro: IPR000194; ATPase_a/bcentre.
DR Pfam: PF00006; ATP-synt_ab; 1.
DR Pfam: PF00306; ATP-synt_ab; 1.
DR Pfam: PF02874; ATP-synt_ab; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
KW Hydrolase; ATP synthetase; Hydrogen ion transport; ATP-binding;
KW Complete proteome.
FT NP_BIND 242 249
SQ SEQUENCE 591 AA; 65301 MW; 7F8432BAB0741B14 CRC64;

Query Match 32.2%; Score 55; DB 1; Length 591;
Best Local Similarity 34.5%; Pred. No. 18;
Matches 10; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 6 MFEELKRMMDVLAQEVALLKEKALQTV 34
D 92 IFDGLQNRLEVLADTSLFKRGEYVNAIC 120

RESULT 8
POLG_HRV14
ID POLG_HRV14 STANDARD; PRT; 2179 AA.
AC P03303; Q82083; Q84736; Q84737; Q84738; Q84739; Q84740;
AC Q84741; Q89441; Q89763; Q89883; Q84774; Q84775; Q84776; Q84777;
AC Q89649; Q84778; Q84779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins
DE P2A TO P2C, P3A; Genome-linked protein VP6; Picornain 3C

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DE (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D
 DE (EC 2.7.7.48)].
 OS Human rhinovirus 14 (HRV-14).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Rhinovirus
 OX NCBI_TaxID=12131;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85037949; PubMed=6093056;
 RA Stanway G., Hughes P.J., Mountford R.C., Minor P.D., Almond J.W.;
 RT "The complete nucleotide sequence of a common cold virus: human
 rhinovirus 14.";
 RL Nucleic Acids Res. 12:7859-7875(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93188162; PubMed=8383233;
 RA Lee W.M., Monroe S., Rueckert R.R.;
 RT "Role of maturation cleavage in infectivity of picornaviruses:
 activation of an Infetosome.";
 RL J. Virol. 67:2110-2122(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85140171; PubMed=2983312;
 RA Callahan P.L., Mizutani S., Colonna R.J.;
 RT "Molecular cloning and complete sequence determination of RNA genome
 of human rhinovirus type 14.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:732-736(1985).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=85296372; PubMed=2993920;
 RA Rossman M.G., Arnold E., Erickson J.W., Frankenberger E.A.,
 RA Griffith J.P., Hecht H.-J., Johnson J.E., Kamer G., Luo M.,
 RA Mosser A.G., Rueckert R.R., Sherry B., Vriend G.;
 RT "Structure of a human common cold virus and functional relationship
 to other picornaviruses.";
 RL Nature 317:145-153(1985).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arnold E., Rossman M.G.;
 RT "The use of molecular-replacement phases for the refinement of the
 human rhinovirus 14 structure.";
 RL Acta Crystallogr. A 44:270-282(1988).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=90189144; PubMed=2156077;
 RA Arnold E., Rossman M.G.;
 RT "Analysis of the structure of a common cold virus, human rhinovirus
 14, refined at a resolution of 3.0 A.";
 RL J. Mol. Biol. 211:763-801(1990).
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
 CC Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.
 CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-I-Gly bond in the
 CC poliovirus polyprotein. In other picornavirus reactions Glu may be
 CC substituted for Gln, and Ser or Thr for Gly.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
 CC -1- CAUTION: THE PDB DATA BANK CONTAINS THE 3D-STRUCTURE COORDINATE
 CC OF PROTEINS VP1, VP2, VP3 AND VP4.
 CC -----
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 CC -----
 CC EMBL; K02121; AAA45756.1; -.

DR EMBL; X01087; CAA25565.1; -.
 DR EMBL; L05355; AAA45758.1; -.
 DR PIR; A03901; GNNYH4.
 DR PDB; 4RHV; 15-OCT-94.
 DR PDB; 1RMU; 15-OCT-94.
 DR PDB; 2RMU; 15-OCT-94.
 DR PDB; 2RM2; 15-OCT-94.
 DR PDB; 2R04; 15-OCT-94.
 DR PDB; 2R06; 15-OCT-94.
 DR PDB; 2R07; 15-OCT-94.
 DR PDB; 1R08; 15-OCT-94.
 DR PDB; 1R09; 15-OCT-94.
 DR PDB; 2RRI; 15-OCT-94.
 DR PDB; 2RS1; 15-OCT-94.
 DR PDB; 2RS3; 15-OCT-94.
 DR PDB; 2RS5; 15-OCT-94.
 DR PDB; 1HRI; 15-OCT-94.
 DR PDB; 2HMB; 01-NOV-94.
 DR PDB; 1HRV; 03-JUN-95.
 DR PDB; 1HVC; 01-NOV-94.
 DR PDB; 1HUC; 14-NOV-95.
 DR PDB; 1RUC; 14-NOV-95.
 DR PDB; 1RUE; 14-NOV-95.
 DR PDB; 1RUF; 14-NOV-95.
 DR PDB; 1RUG; 14-NOV-95.
 DR PDB; 1RUH; 14-NOV-95.
 DR PDB; 1RUI; 14-NOV-95.
 DR PDB; 1RUJ; 14-NOV-95.
 DR PDB; 1RVP; 25-FEB-98.
 DR PDB; 1VRH; 12-FEB-97.
 DR MEROPS; C03.UBA; -.
 DR MEROPS; C03.UPB; -.
 DR InterPro; IPR000199; Cys-protease-3C.
 DR InterPro; IPR003138; Pico_P1A.
 DR InterPro; IPR000081; Pico_P2A.
 DR InterPro; IPR002527; Pico_P2B.
 DR InterPro; IPR000605; RNA_helicase.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR001676; Rhv.
 DR Pfam; PF00073; rhv; 3.
 DR Pfam; PF00548; Cys-protease-3C; 1.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00910; RNA_helicase; 1.
 DR Pfam; PF00947; Pico_P2A; 1.
 DR Pfam; PF01552; Pico_P2B; 1.
 DR Pfam; PF02226; Pico_P1A; 1.
 DR ProDom; PD001125; Cys-protease-3C; 1.
 DR ProDom; PD001274; Pico_P2B; 1.
 DR ProDom; PD001306; Pico_P2A; 1.
 KW Polyprotein; Coat protein; Core protein; Transferase;
 KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate;
 KW 3D-structure.
 FT CHAIN 2 69 COAT PROTEIN VP4 (PIA).
 FT CHAIN 70 331 COAT PROTEIN VP2 (PIB).
 FT CHAIN 332 567 COAT PROTEIN VP3 (PIC).
 FT CHAIN 568 856 COAT PROTEIN VP1 (PID).
 FT CHAIN 857 1002 CORE PROTEIN P2A.
 FT CHAIN 1003 1099 CORE PROTEIN P2B.
 FT CHAIN 1100 1429 CORE PROTEIN P2C.
 FT CHAIN 1430 1514 CORE PROTEIN P3A.
 FT CHAIN 1515 1537 GENOME-LINKED PROTEIN VPG (P3B).
 FT CHAIN 1538 1719 PICORNAIN 3C.
 FT CHAIN 1720 2179 RNA-DIRECTED RNA POLYMERASE P3D.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT ACT_SITE 1683 1683 PROTEASE (POTENTIAL).
 FT ACT_SITE 1697 1697 PROTEASE (POTENTIAL).
 FT CONFLICT 368 368 P -> L (IN REF. 3).
 FT CONFLICT 459 459 I -> T (IN REF. 3).
 FT CONFLICT 722 722 P -> H (IN REF. 3).
 FT CONFLICT 726 727 NP -> KS (IN REF. 3).
 FT CONFLICT 729 731 EWD -> RVG (IN REF. 3).
 FT CONFLICT 731 913 C -> R (IN REF. 3).
 FT CONFLICT 913 942 N -> S (IN REF. 3).
 FT CONFLICT 942 942

[illegible]

FT DOMAIN 811 830 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 831 853 POTENTIAL.
FT DOMAIN 854 905 LUMENAL (POTENTIAL).
FT TRANSMEM 906 925 POTENTIAL.
FT DOMAIN 926 938 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 939 957 POTENTIAL.
FT DOMAIN 958 972 LUMENAL (POTENTIAL).
FT TRANSMEM 973 993 POTENTIAL.
FT DOMAIN 994 1010 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 363 363 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 930 930 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT BINDING 69 71 BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY SIMILARITY).
FT METAL 704 704 MAGNESIUM (BY SIMILARITY).
FT METAL 708 708 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 1010 AA; 111284 MW; 715266BC2563BFA6 CRC64;

Query Match 30.4%; Score 52; DB 1; Length 1010;
Best Local Similarity 38.5%; Pred. No. 73;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Oy 11 KNRMDVLAQEVALLKEKQALQTVCLK 36
Db 16 KRDDDLKKEVAMTEHKMSIEVCCK 41

RESULT 15

MCAL_CRIGR STANDARD; PRT; 359 AA.
AC 054873;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multisynthetase complex auxiliary component P43 [Contains:
DE Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
DE Inducible cytokine subfamily E member 1)].
GN SCYE1.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98070438; PubMed=9405472;
RA Quevillon S., Agou F., Robinson J.-C., Mirande M.
RT "The P43 component of the mammalian multi-synthetase complex is likely
RT to be the precursor of the endothelial monocyte-activating polypeptide
RT II cytokine.";
RL J. Biol. Chem. 272:32573-32579(1997).
CC -!- SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS
CC COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE
CC MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LYSYL,
CC ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY
CC PROTEINS, P18, P48 AND P43.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF021800; AAB95207.1; -
DR InterPro: IPR002547; trna_bind.
DR Pfam: PF01588; trna_bind; 1.
KW Protein biosynthesis; trna-binding; Cytokine.
FT DOMAIN 204 297 TRNA BINDING.
SQ SEQUENCE 359 AA; 39601 MW; 4D868D1B65D72C23 CRC64;

Query Match 29.8%; Score 51; DB 1; Length 359;
Best Local Similarity 61.1%; Pred. No. 34;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Oy 14 MDVLAQEVALLKEKQALQ 31
Db 68 IEYLKQVALLKEKRAVLQ 85

Search completed: April 15, 2003, 11:48:32
Job time : 8.5 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:44 ; Search time 11.75 seconds
(without alignments)
294,540 Million cell updates/sec

Title: US-09-445-576A-37
Perfect score: 171
Sequence: 1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLX 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	202	2 JC4031	tetranectin precu
2	146	85.4	202	1 TTHUN	tetranectin precu
3	89	52.0	166	1 A37289	tetranectin homolo
4	56.5	33.0	323	2 T07734	homeotic protein v
5	55	32.2	224	2 S56809	probable membrane
6	55	32.2	524	2 S75852	hypothetical prote
7	55	32.2	591	2 E81687	ATP synthase, chai
8	55	32.2	857	2 F81396	ATP-dependent CLP
9	55	32.2	2179	1 GNNTH4	genome polyprotein
10	54	31.6	761	2 T03719	probable thyroid r
11	54	31.6	1549	2 T21809	hypothetical prote
12	54	31.6	1893	2 T22661	hypothetical prote
13	54	31.6	1957	2 T38077	hypothetical coile
14	54	31.6	2823	2 T23064	hypothetical prote
15	54	31.6	2823	2 F87908	protein T22A3.8 [1
16	54	31.6	3102	2 T43291	laminin alpha chai
17	53.5	31.3	403	2 C64998	hypothetical prote
18	53.5	31.3	513	2 T10830	nitrogenase (EC 1.
19	53.5	31.3	1014	2 T30840	serine-repeat anti
20	53	31.0	908	2 AH1722	hypothetical prote
21	53	31.0	1660	2 A84647	hypothetical prote
22	52	30.4	168	2 T08831	disease resistance
23	52	30.4	213	2 E83972	hypothetical prote
24	52	30.4	425	2 H83652	seryl-tRNA synthet
25	52	30.4	486	2 B84914	hypothetical prote
26	52	30.4	609	2 AB3288	ABC transporter AT
27	52	30.4	852	2 D72330	conserved hypothet
28	52	30.4	1010	2 B37227	Na+/K+-exchanging
29	51.5	30.1	381	2 A54415	transcription fact

30	51.5	30.1	407	2 E91023	probable sulfatase
31	51.5	30.1	407	2 F85867	probable sulfatase
32	51.5	30.1	833	2 H72205	maltose ABC transp
33	51	29.8	69	2 T43093	hypothetical prote
34	51	29.8	219	2 S46526	MADS box protein m
35	51	29.8	498	2 A10458	conserved hypothet
36	51	29.8	513	1 B23874	nitrogenase (EC 1.
37	51	29.8	591	2 B71531	probable ATP synth
38	51	29.8	1013	2 C24639	Na+/K+-exchanging
39	51	29.8	1548	2 T25808	hypothetical prote
40	51	29.8	2342	2 T18200	fatty-acid synthas
41	50.5	29.5	316	2 C70438	conserved hypothet
42	50.5	29.5	799	2 T02456	protein kinase hom
43	50.5	29.5	4367	1 B54802	dynein heavy chain
44	50	29.2	90	2 E86899	conserved hypothet
45	50	29.2	310	2 A55053	endothelial monocy

ALIGNMENTS

RESULT 1
JC4031
tetranectin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C:Accession: JC4031
R:Sorensen, C.B.; Berglund, L.; Petersen, T.E.
Gene 152, 243-245, 1995
A:Title: Cloning of a cDNA encoding murine tetranectin.
A:Reference number: JC4031; MUID:95137396; PMID:7835708
A:Accession: JC4031
A:Molecule type: mRNA
A:Residues: 1-202 <SOR>
A:Cross-references: EMBL:X79199; MID:9671561; PIDN:CAA555791.1; PID:9671562
A:Experimental source: lung
C:Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C:Superfamily: tetranectin; C-type lectin homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-202/Product: tetranectin #status predicted <MAT>
F:71-197/Domain: C-type lectin homology <ICH>

Query Match 100.0%; Score 171; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLX 36
|||||
Db 38 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLX 73

RESULT 2
TTHUN
tetranectin precursor [validated] - human
N:Alternate names: plasminogen-kringle 4 binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 03-Aug-1995 #text_change 08-Dec-2000
C:Accession: S24126; A56835; A29747; I38359; S19865
R:Berglund, L.; Petersen, T.E.
FEBS Lett. 309, 15-19, 1992
A:Title: The gene structure of tetranectin, a plasminogen binding protein.
A:Reference number: S24126; MUID:92380263; PMID:1511740
A:Accession: S24126
A:Molecule type: DNA
A:Residues: 1-202 <BER>
A:Cross-references: EMBL:X70911
R:Wewer, U.M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992

A:Title: Tetranectin, a plasminogen kringle 4-binding protein.. Cloning and gene expre
A:Reference number: A56835; MUID:92365345; PMID:1354271
A:Accession: A56835
A:Molecule type: mRNA
A:Residues: 1-202 <WED>

A:Molecule type: mRNA
A:Residues: 1-323 <TOW>
A:CROSS-references: EMBL:X94947; NID:g1l61574; PIDN:CAA64417.1; PID:gl161575
A:Experimental source: cultivar VFN8; leaf
C:Genetics:
A:Gene: VAHOX1
A:Introns: 49/3; 178/3
A>Note: specifically expressed in the phloem during phases of secondary growth
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:88-144/Domain: homeobox homology <Hox>

Query Match 33.0%; Score 56.5; DB 2; Length 323;
Best Local Similarity 48.3%; Pred. No. 13;
Matches 14; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

OY 5 KMFEELKNRMDVLAQEV-ALLKEKQALQT 32
| :||| | | | ||||| :|
Db 149 KDYDELNRNYDTLKSNYNLLKEKD LRT 177

RESULT 5
S56809
probable membrane protein YJL037w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein J1234
C:Species: *Saccharomyces cerevisiae*
C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C:Accession: S56809
R:Pohl, T.M.; Aljinovic, G.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56793
A:Accession: S56809
A:Molecule type: DNA
A:Residues: 1-224 <TOV>
A:CROSS-references: EMBL:Z49312; NID:g1008160; PID:g1008161; GSPDB:GN00010; MIPS:YLJO
C:Genetics:
A:Gene: MIPS:YJL037w
A:CROSS-references: SGD:S0003574
A:Map position: 10L
C:Keywords: transmembrane protein

Query Match 32.2%; Score 55; DB 2; Length 224;
Best Local Similarity 44.4%; Pred. No. 14;
Matches 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 2 VSSKMFEELKNRMDVLAQEVALLKEKQ 28
| :||| | | | ||||| :|
Db 136 VSTKKFESLLNKYDLVAKKGGELTEEQ 162

RESULT 6
S75852
hypothetical protein sll1433 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75852
R:kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75852
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-524 <KAN>
A:CROSS-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18311.1; PID:g165
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Thermotoga maritima hypothetical protein MTH1256

Query Match 32.2%; Score 55; DB 2; Length 524;
Best Local Similarity 40.6%; Pred. No. 34;

QY	5	KMFEELKN--RMDVLAQEVALKEKQ	28
Dh	430	KMNDEKNOKRIDETAKETANI,KEQ	455

C;Accession: T21809

R:Chui, C.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19473
A:Accession: T21809
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1549 <WIL>
A:Cross-references: EMBL:Z46242; PIDN:CAA86336.1; GSPDB:GN00021; CESP:F35G12.8
A:Experimental source: clone F35G12
C:Genetics:
A:Gene: CESP:F35G12.8
A:Map position: 3
A:Introns: 50/3; 72/3; 177/3; 235/3; 333/2; 581/3; 667/3; 812/3; 882/1; 1050/3; 1223/3;
C:Superfamily: chromosome segregation protein SMC1

Query Match 31.6%; Score 54; DB 2; Length 1549;
Best Local Similarity 44.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 5 KMFEELKNRMDVLAQAEVALLKEKQA 29
DB 874 KIVELEKRRDELGEAAKVKRQA 898
I: |||: | | | | | | | | | |
I: |||: | | | | | | | | | |

RESULT 12
T22661
hypothetical protein T01G1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T22661; T24305
R:White, S.; Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19594
A:Accession: T22661
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1893 <WIL>
A:Cross-references: EMBL:Z82271; PIDN:CAB05214.1; GSPDB:GN00022; CESP:T01G1.1
A:Experimental source: clone F54E12
R:Kershaw, J.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19872
A:Accession: T24305
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1893 <WIL>
A:Cross-references: EMBL:Z92811; PIDN:CAB07273.1; GSPDB:GN00022; CESP:T01G1.1
A:Experimental source: clone T01G1
C:Genetics:
A:Gene: CESP:T01G1.1
A:Map position: 4
A:Introns: 65/3; 101/3; 194/3; 269/3; 299/2; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1; 9

Query Match 31.6%; Score 54; DB 2; Length 1893;
Best Local Similarity 48.4%; Pred. No. 1.8e+02;
Matches 15; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 3 SSKMFEELKNRMDVLAQAEVALLKEKQALQTV 33
DB 657 SSKMIGELRSR--IAALEALLEFKGRRTV 685
I: |||: |||: | | | | | | | | | |
I: |||: |||: | | | | | | | | | |

RESULT 13
T38077
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38077
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z21767
A:Accession: T38077
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1957 <CON>
A:Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A:Experimental source: strain 972h; cosmid cif3
C:Genetics:
A:Gene: SPDB:SPAC1F3.06c
A:Map position: 1

Query Match 31.6%; Score 54; DB 2; Length 1957;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 6; Mismatches 3; Indels 4; Gaps 1;

QY 9 ELKNRMDVLAQAEVALLKEKQAL 30
DB 1394 KLNQDLHNLQELRLKEDVLKEKESL 1419
I: |||: | | | | | | | | | |
I: |||: | | | | | | | | | |

RESULT 14
T23064
hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T23064; T25096
R:Barlow, K.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19669
A:Accession: T23064
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2823 <WIL>
A:Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
A:Experimental source: clone H10E24
R:McMurray, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19980
A:Accession: T25096
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2823 <WIL>
A:Cross-references: EMBL:Z81125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A:Experimental source: clone T22A3
C:Genetics:
A:Gene: CESP:T22A3.8
A:Map position: 1
A:Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-lik

Query Match 31.6%; Score 54; DB 2; Length 2823;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSKMFEELKNRMDVLAQ 19
DB 1874 LNETIFEDLKNRIDVLEQ 1891
I: |||: |||: | | | | | | | | | |
I: |||: |||: | | | | | | | | | |

RESULT 15
F87908
protein T22A3.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C:Accession: F87908; E87908
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:90069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: F87908
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <STO>
A:Cross-references: GB:chr_I; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A

A:Accession: E87908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2823 <ST2>
A:Cross-references: GB:chr_1; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
C:Genetics:
A:Gene: T22A3.8
A:Map position: 1
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like F
Query Match 31.6%; Score 54; DB 2; Length 2823;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 2 VSSKNFEEELKNRMVLAQ 19
:: :||:|||||
Db 1874 LNETIFEDLKNRIDVLEQ 1891
Search completed: April 15, 2003, 11:51:04
Job time : 13.75 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:39 ; Search time 23.25 seconds
(without alignments)
241.276 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSSKMFEEELKRMVDVLAQEVALLKEKQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 704857 seqs, 155824263 residues

Total number of hits satisfying chosen parameters: 704857

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	171	100.0	36	5	US-09-445-576A-37
2	146	85.4	36	5	US-09-445-576A-36
3	146	85.4	52	5	US-09-445-576A-71
4	146	85.4	180	5	US-09-445-576A-27
5	146	85.4	181	5	US-09-445-576A-7
6	146	85.4	197	5	US-09-445-576A-25
7	146	85.4	202	1	PCT-US02-38407-13
8	146	85.4	202	5	US-09-992-0958-62
9	146	85.4	202	5	US-09-999-570-62
10	146	85.4	202	6	US-10-154-678-62
11	146	85.4	202	6	US-10-276-781-1559
12	146	85.4	228	5	US-09-445-576A-24
13	141	82.5	51	5	US-09-445-576A-35
14	136	79.5	52	5	US-09-445-576A-5
15	136	79.5	73	5	US-09-445-576A-28
16	128	74.9	49	5	US-09-445-576A-6
17	128	74.9	65	5	US-09-445-576A-26
18	124	72.5	65	5	US-09-445-576A-29
19	124	72.5	145	5	US-09-445-576A-31
20	124	72.5	330	5	US-09-445-576A-32
21	124	72.5	331	5	US-09-445-576A-33
22	124	72.5	592	5	US-09-445-576A-34
23	89	52.0	36	5	US-09-445-576A-39
24	82	48.0	59	5	US-09-513-999C-4342
25	76	44.4	36	5	US-09-445-576A-38
26	72	42.1	197	1	PCT-US02-19669A-55

27	72	42.1	206	1	PCT-US02-19669A-57	Sequence 57, Appl
28	72	42.1	206	5	US-09-989-733-403	Sequence 403, App
29	72	42.1	206	5	US-09-992-643-403	Sequence 403, App
30	72	42.1	206	6	US-10-125-923A-276	Sequence 276, App
31	72	42.1	206	6	US-10-205-892-276	Sequence 276, App
32	72	42.1	206	6	US-10-174-575-276	Sequence 276, App
33	72	42.1	206	6	US-10-174-575A-276	Sequence 276, App
34	72	42.1	206	6	US-10-187-755-276	Sequence 276, App
35	72	42.1	206	6	US-10-187-749-276	Sequence 276, App
36	72	42.1	206	6	US-10-199-672-276	Sequence 276, App
37	72	42.1	206	6	US-10-194-486-276	Sequence 276, App
38	64	37.4	36	5	US-09-445-576A-40	Sequence 40, Appl
39	59	34.5	370	6	US-10-282-122A-45353	Sequence 45353, A
40	56	32.7	669	7	US-60-453-135-8627	Sequence 8627, Ap
41	56	32.7	669	7	US-60-453-050-8627	Sequence 8627, Ap
42	55	32.2	857	6	US-10-282-122A-54349	Sequence 54349, A
43	55	32.2	1178	6	US-10-282-122A-72168	Sequence 72168, A
44	54.5	31.9	519	6	US-10-369-493-20472	Sequence 20472, A
45	54	31.6	751	6	US-10-203-138A-15377	Sequence 15377, A

ALIGNMENTS

RESULT 1
US-09-445-576A-37
; Sequence 37, Application US/09445576A.
; GENERAL INFORMATION:
; APPLICANT: Borean Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445.576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Murine
US-09-445-576A-37

Query Match 100.0%; Score 171; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVSSKMFEEELKRMVDVLAQEVALLKEKQALQTVCLK 36
Db 1 LVSSKMFEEELKRMVDVLAQEVALLKEKQALQTVCLK 36

RESULT 2
US-09-445-576A-36
; Sequence 36, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Borean Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445.576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-445-576A-36

Query Match 85.4%; Score 146; DB 5; Length 36;
Best Local Similarity 80.6%; Pred. No. 1.1e-14;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVSSKMFEEELKRMVDVLAQEVALLKEKQALQTVCLK 36
Db 1 LVSSKMFEEELKRMVDVLAQEVALLKEKQALQTVCLK 36

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Db 1 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 36
; OTHER INFORMATION: Mature tetranectin single chain
; US-09-445-576A-7
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; Query Match 85.4%; Score 146; DB 5; Length 181;
; Best Local Similarity 80.6%; Pred. No. 9e-14;
; Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 LVSSKMFELKRNMDVLAQEVALLKEQALQTVCLK 36
; Db 17 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 52
;
; RESULT 6
; US-09-445-576A-25
; Sequence 25, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: H6FXTN123
; US-09-445-576A-25
;
; Query Match 85.4%; Score 146; DB 5; Length 197;
; Best Local Similarity 80.6%; Pred. No. 1e-13;
; Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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; QY 1 LVSSKMFELKRNMDVLAQEVALLKEQALQTVCLK 36
; Db 33 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 68
;
; RESULT 7
; PCT-US02-38407-13
; Sequence 13, Application PC/TUS0238407
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPME
; TITLE OF INVENTION: OSTEOARTHRITIS
; FILE REFERENCE: D0189
; CURRENT APPLICATION NUMBER: PCT/US02/38407
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,417
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PCT-US02-38407-13
;
; Query Match 85.4%; Score 146; DB 1; Length 202;
; Best Local Similarity 80.6%; Pred. No. 1e-13;
; Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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; QY 1 LVSSKMFELKRNMDVLAQEVALLKEQALQTVCLK 36
; Db 38 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 73
;
; RESULT 8
; US-09-992-095B-62
; Sequence 62, Application US/09992095B
; GENERAL INFORMATION:
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Db 1 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 36
; OTHER INFORMATION: Mature tetranectin single chain
; US-09-445-576A-7
;
; Query Match 85.4%; Score 146; DB 5; Length 181;
; Best Local Similarity 80.6%; Pred. No. 1.8e-14;
; Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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; QY 1 LVSSKMFELKRNMDVLAQEVALLKEQALQTVCLK 36
; Db 17 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 52
;
; RESULT 4
; US-09-445-576A-27
; Sequence 27, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: H6FXTN23
; US-09-445-576A-27
;
; Query Match 85.4%; Score 146; DB 5; Length 180;
; Best Local Similarity 80.6%; Pred. No. 9e-14;
; Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 LVSSKMFELKRNMDVLAQEVALLKEQALQTVCLK 36
; Db 16 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 51
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; RESULT 5
; US-09-445-576A-7
; Sequence 7, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91 US5 DIV
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 62
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..21
US-09-992-095B-62

Query Match 85.4%; Score 146; DB 5; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-13;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LVSSKMFEEELKRNMDVLAQEAVALLEKEQALQTVCLK 36
Db 38 VVNTKMFEEELKSRDLTLAQEAVALLEKEQALQTVCLK 73

RESULT 9
US-09-999-570-62
Sequence 62, Application US/09999570
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US08DIV
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 62
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..21
US-09-999-570-62

Query Match 85.4%; Score 146; DB 5; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-13;

Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LVSSKMFEEELKRNMDVLAQEAVALLEKEQALQTVCLK 36
Db 38 VVNTKMFEEELKSRDLTLAQEAVALLEKEQALQTVCLK 73
RESULT 10
US-10-154-678-62
Sequence 62, Application US/10154678
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182 US1 REG
CURRENT APPLICATION NUMBER: US/10/154,678
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 62
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -21...-1
US-10-154-678-62

Query Match 85.4%; Score 146; DB 6; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-13;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LVSSKMFEEELKRNMDVLAQEAVALLEKEQALQTVCLK 36
Db 38 VVNTKMFEEELKSRDLTLAQEAVALLEKEQALQTVCLK 73

RESULT 11
US-10-276-781-1559
Sequence 1559, Application US/10276781
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1559
LENGTH: 202
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-781-1559

Query Match 85.4%; Score 146; DB 6; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-13;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LVSSKMFEEELKRNMDVLAQEAVALLEKEQALQTVCLK 36
Db 38 VVNTKMFEEELKSRDLTLAQEAVALLEKEQALQTVCLK 73

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US-09-445-576A-5
; Sequence 5, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 6202.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:05 ; Search time 183 Seconds
(without alignments)
126.833 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSSKMFELKRMVDLAQEVALLKEKQALQTVCLK 36

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
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- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
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- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
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- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	36	18 US-09-445-576-36	Sequence 36, Appl
2	171	100.0	36	23 US-09-987-107-40	Sequence 40, Appl
3	171	100.0	202	21 US-09-791-537-28929	Sequence 28929, A
4	171	100.0	202	21 US-09-791-537-40295	Sequence 40295, A
5	146	85.4	36	18 US-09-445-576-35	Sequence 35, Appl
6	146	85.4	36	23 US-09-987-107-39	Sequence 39, Appl

7	146	85.4	95	22	US-09-834-366-13425	Sequence 13425, A
8	146	85.4	95	27	US-60-197-873-13425	Sequence 13425, A
9	146	85.4	180	18	US-09-445-576-27	Sequence 27, Appl
10	146	85.4	181	18	US-09-445-576-7	Sequence 7, Appl
11	146	85.4	197	18	US-09-445-576-25	Sequence 25, Appl
12	146	85.4	202	21	US-09-791-537-41342	Sequence 41342, A
13	146	85.4	202	23	US-09-924-340-62	Sequence 62, Appl
14	146	85.4	202	23	US-09-992-600A-62	Sequence 62, Appl
15	146	85.4	202	23	US-09-994-590-62	Sequence 62, Appl
16	146	85.4	202	24	US-10-000-489-62	Sequence 62, Appl
17	146	85.4	202	24	US-10-000-986-62	Sequence 62, Appl
18	146	85.4	202	27	US-60-305-456-62	Sequence 62, Appl
19	146	85.4	202	27	US-60-365-384-579	Sequence 579, Appl
20	146	85.4	228	18	US-09-445-576-24	Sequence 24, Appl
21	146	85.4	254	26	US-10-238-659-667	Sequence 667, App
22	146	85.4	268	26	US-10-238-659-450	Sequence 450, App
23	143	83.6	182	21	US-09-791-537-88542	Sequence 88542, A
24	141	82.5	51	23	US-09-987-107-12	Sequence 12, Appl
25	136	79.5	52	18	US-09-445-576-5	Sequence 5, Appl
26	136	79.5	58	23	US-09-987-107-13	Sequence 13, Appl
27	136	79.5	73	18	US-09-445-576-28	Sequence 28, Appl
28	136	79.5	258	23	US-09-987-107-4	Sequence 4, Appl
29	136	79.5	273	23	US-09-987-107-50	Sequence 50, Appl
30	136	79.5	301	23	US-09-987-107-3	Sequence 3, Appl
31	136	79.5	301	23	US-09-987-107-5	Sequence 5, Appl
32	136	79.5	304	23	US-09-987-107-6	Sequence 6, Appl
33	136	79.5	304	23	US-09-987-107-7	Sequence 7, Appl
34	136	79.5	304	23	US-09-987-107-8	Sequence 8, Appl
35	136	79.5	306	23	US-09-987-107-9	Sequence 9, Appl
36	136	79.5	306	23	US-09-987-107-10	Sequence 10, Appl
37	136	79.5	306	23	US-09-987-107-11	Sequence 11, Appl
38	136	79.5	316	23	US-09-987-107-48	Sequence 48, Appl
39	136	79.5	316	23	US-09-987-107-54	Sequence 54, Appl
40	136	79.5	323	23	US-09-987-107-56	Sequence 56, Appl
41	136	79.5	323	23	US-09-987-107-58	Sequence 58, Appl
42	136	79.5	323	23	US-09-987-107-60	Sequence 60, Appl
43	136	79.5	324	23	US-09-987-107-62	Sequence 62, Appl
44	136	79.5	324	23	US-09-987-107-64	Sequence 64, Appl
45	136	79.5	324	23	US-09-987-107-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-445-576-36
; Sequence 36, Application US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Heilskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjoller
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN -1
; CURRENT APPLICATION NUMBER: US/09/445,576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 36
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Murine
US-09-445-576-36

Query Match 100.0%; Score 171; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.6e-16;

; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-39

Query Match 85.4%; Score 146; DB 23; Length 36;
Best Local Similarity 80.6%; Pred. No. 1.1e-12;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Db 1 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVCLK 36

RESULT 7
US-09-834-366-13425
; Sequence 13425, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834.366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13425
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-834-366-13425

Query Match 85.4%; Score 146; DB 22; Length 95;
Best Local Similarity 80.6%; Pred. No. 3.9e-12;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRNMDVLAQAEVALLKEQALQTVCLK 36
:|::|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 38 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVCLK 73

RESULT 8
US-60-197-873-13425
; Sequence 13425, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197.873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 13425
; LENGTH: 95

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-60-197-873-13425

Query Match 85.4%; Score 146; DB 27; Length 95;
Best Local Similarity 80.6%; Pred. No. 3.9e-12;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRNMDVLAQAEVALLKEQALQTVCLK 36
:|::|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 38 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVCLK 73

RESULT 9
US-09-445-576-27
; Sequence 27, Application US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Hellskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjolier
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN =1
; CURRENT APPLICATION NUMBER: US/09/445.576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H6FXTN23
US-09-445-576-27

Query Match 85.4%; Score 146; DB 18; Length 180;
Best Local Similarity 80.6%; Pred. No. 9e-12;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRNMDVLAQAEVALLKEQALQTVCLK 36
:|::|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 16 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVCLK 51

RESULT 10
US-09-445-576-7
; Sequence 7, Application US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Hellskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjolier
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN =1
; CURRENT APPLICATION NUMBER: US/09/445.576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11

; ORGANISM: Homo sapiens

6.

; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; US-09-992-600A-62

Query Match 85.4%; Score 146; DB 23; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-11; Indels 0; Gaps 0;
Matches 29; Conservative 6; Mismatches 1;

Oy 1 LVSSKMFEEKNRMDVLAQEVALLKEQALQTVCLK 36
:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 38 VVNTKMFEEKSRDLTLAQEVALLKEQALQTVCLK 73

RESULT 15
US-09-994-590-62
; Sequence 62, Application US/09994590
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US3.DIV
; CURRENT APPLICATION NUMBER: US/09/994,590
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; US-09-994-590-62

Query Match 85.4%; Score 146; DB 23; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-11; Indels 0; Gaps 0;
Matches 29; Conservative 6; Mismatches 1;

Oy 1 LVSSKMFEEKNRMDVLAQEVALLKEQALQTVCLK 36
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Db 38 VVNTKMFEEKSRDLTLAQEVALLKEQALQTVCLK 73

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Job time : 183 secs

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:50:25 ; Search time 10 seconds
(without alignments)
220.090 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSSKMFELKRMVDVLAQEVALLKEKQALQTVCLK 36

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Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	146	85.4	36	9	US-09-987-107-39
3	146	85.4	202	9	US-09-924-340-62
4	146	85.4	202	9	US-09-992-600A-62
5	141	82.5	51	9	US-09-987-107-12
6	136	79.5	58	9	US-09-987-107-13
7	136	79.5	258	9	US-09-987-107-4
8	136	79.5	273	9	US-09-987-107-50
9	136	79.5	301	9	US-09-987-107-3
10	136	79.5	301	9	US-09-987-107-5
11	136	79.5	304	9	US-09-987-107-6
12	136	79.5	304	9	US-09-987-107-7
13	136	79.5	304	9	US-09-987-107-8
14	136	79.5	306	9	US-09-987-107-9
15	136	79.5	306	9	US-09-987-107-10
16	136	79.5	306	9	US-09-987-107-11
17	136	79.5	316	9	US-09-987-107-48
18	136	79.5	316	9	US-09-987-107-54
19	136	79.5	323	9	US-09-987-107-56

20	136	79.5	323	9	US-09-987-107-58
21	136	79.5	323	9	US-09-987-107-60
22	136	79.5	324	9	US-09-987-107-62
23	136	79.5	324	9	US-09-987-107-64
24	136	79.5	324	9	US-09-987-107-66
25	89	52.0	36	9	US-09-987-107-42
26	76	44.4	36	9	US-09-987-107-41
27	72	42.1	197	10	US-09-745-288-99
28	72	42.1	206	9	US-09-938-418-10
29	72	42.1	206	9	US-09-982-598-403
30	72	42.1	206	9	US-09-989-293A-403
31	72	42.1	206	9	US-09-989-735-403
32	72	42.1	206	9	US-09-990-444-403
33	72	42.1	206	9	US-09-989-730-403
34	72	42.1	206	9	US-09-990-436-403
35	72	42.1	206	9	US-09-991-181-403
36	72	42.1	206	9	US-09-993-687-403
37	72	42.1	206	9	US-09-989-734-403
38	72	42.1	206	9	US-10-127-966-2
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40	72	42.1	206	9	US-10-174-590-276
41	72	42.1	206	9	US-10-176-758-276
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43	72	42.1	206	9	US-09-993-667-403
44	72	42.1	206	9	US-10-173-706-276
45	72	42.1	206	9	US-10-175-738-276

ALIGNMENTS

RESULT 1

US-09-987-107-40
; Sequence 40, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-987-107-40

Query Match 100.0%; Score 171; DB 9; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.6e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMVDVLAQEVALLKEKQALQTVCLK 36
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Db 1 LVSSKMFELKRMVDVLAQEVALLKEKQALQTVCLK 36

RESULT 2

US-09-987-107-39
; Sequence 39, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES

DB 17 VYNTKFEELKSRDLT LAQEVALLKEQALQTVCL 51

RESULT 6
US-09-987-107-13
; Sequence 13, Application US/09987107
; Patent No. US20020156007A1

Query Match 79.5%; Score 136; DB 9; Length 258;

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RESULT 9
US-09-987-107-3
; Sequence 3, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc.feature
; LOCATION: (59)..(301)

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; OTHER INFORMATION: Mature ApoA1
; US-09-987-107-3
Query Match          79.5%; Score 136; DB 9; Length 301;
Best Local Similarity 77.8%; Pred. No. 1.3e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56

RESULT 10
US-09-987-107-5
; Sequence 5, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: Mutagen
; NAME/KEY: misc_feature
; LOCATION: (59)..(301)
; OTHER INFORMATION: Apo-A1 mature
; US-09-987-107-5
Query Match          79.5%; Score 136; DB 9; Length 301;
Best Local Similarity 77.8%; Pred. No. 1.3e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56

RESULT 11
US-09-987-107-6
; Sequence 6, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Fibronectin based linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
; US-09-987-107-7
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Best Local Similarity 77.8%; Pred. No. 1.4e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56

RESULT 12
US-09-987-107-7
; Sequence 7, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Fibronectin based linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
; US-09-987-107-7
Query Match          79.5%; Score 136; DB 9; Length 304;
Best Local Similarity 77.8%; Pred. No. 1.4e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56
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; OTHER INFORMATION: Mature ApoA1
; US-09-987-107-3
Query Match          79.5%; Score 136; DB 9; Length 301;
Best Local Similarity 77.8%; Pred. No. 1.3e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56

RESULT 10
US-09-987-107-5
; Sequence 5, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 301
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; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(58)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: Mutagen
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: Mutagen
; NAME/KEY: misc_feature
; LOCATION: (59)..(301)
; OTHER INFORMATION: Apo-A1 mature
; US-09-987-107-5
Query Match          79.5%; Score 136; DB 9; Length 301;
Best Local Similarity 77.8%; Pred. No. 1.3e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56

RESULT 11
US-09-987-107-6
; Sequence 6, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(56)
; OTHER INFORMATION: Trimerisation module from tetranectin
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Fibronectin based linker
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
; US-09-987-107-7
Query Match          79.5%; Score 136; DB 9; Length 304;
Best Local Similarity 77.8%; Pred. No. 1.4e-10;
Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LVSSKMFELKRMNDVLAQAEVALLKEQALQTVCLK 36
Db 21 VVNTKMFELKSRDLTLAQAEVALLKEQALQTVSLK 56
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Job time : 11 secs

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Copyright (c) 1993 - 2003 CompuGen Ltd.

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(without alignments)
105.923 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSSKMFELKRMVDVLAQVEALLKQALQTVCLK 36,

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	85.4	202	1	US-08-469-486-56
2	146	85.4	202	2	US-08-469-658-56
3	72	42.1	197	4	US-09-602-877A-99
4	51	29.8	802	4	US-09-156-316-1
5	50	29.2	310	1	US-08-129-456A-36
6	50	29.2	310	2	US-08-705-868-3
7	50	29.2	310	3	US-09-123-615-3
8	50	29.2	310	4	US-08-360-821B-35
9	50	29.2	528	4	US-08-928-213B-8
10	50	29.2	1358	1	US-08-404-665-4
11	50	29.2	1358	1	US-08-404-671-4
12	50	29.2	1358	1	US-08-404-781-4
13	49	28.7	835	2	US-08-968-751-4
14	48	28.1	77	1	US-08-178-477B-29
15	48	28.1	691	1	US-08-178-477B-2
16	48	28.1	1066	4	US-09-541-782-8
17	48	28.1	1066	4	US-09-723-820-8
18	48	28.1	3066	4	US-08-952-127-12
19	47.5	27.8	718	3	US-09-090-808-2
20	47.5	27.8	718	4	US-09-447-453-2
21	47.5	27.8	1232	4	US-09-592-054-2
22	47.5	27.8	1279	4	US-09-724-517-2
23	47.5	27.8	1279	4	US-09-641-807A-2
24	47.5	27.8	1279	4	US-09-723-096-2
25	47	27.5	310	1	US-08-129-456A-37
26	47	27.5	312	4	US-08-360-821B-36
27	46.5	27.2	1010	4	US-09-134-001C-5178

28	46	26.9	98	2	US-08-690-011A-19	Sequence 19, Appl
29	46	26.9	276	4	US-08-659-254-2	Sequence 2, Appl
30	46	26.9	284	2	US-08-538-960-2	Sequence 2, Appl
31	46	26.9	504	2	US-08-645-900A-1	Sequence 1, Appl
32	46	26.9	504	2	US-08-882-238A-1	Sequence 1, Appl
33	46	26.9	504	2	US-08-667-790A-1	Sequence 1, Appl
34	46	26.9	504	4	US-09-220-459-1	Sequence 1, Appl
35	46	26.9	504	4	US-08-938-669A-32	Sequence 32, Appl
36	46	26.9	504	4	US-08-546-568B-1	Sequence 1, Appl
37	46	26.9	504	4	US-09-056-285A-8	Sequence 8, Appl
38	46	26.9	1024	4	US-09-562-737-86	Sequence 86, Appl
39	45.5	26.6	40	1	US-08-467-943-2	Sequence 2, Appl
40	45.5	26.6	42	2	US-07-801-798-5	Sequence 5, Appl
41	45.5	26.6	42	5	PCT-US92-10140-5	Sequence 5, Appl
42	45.5	26.6	49	2	US-08-256-790-14	Sequence 14, Appl
43	45.5	26.6	53	2	US-08-256-790-10	Sequence 10, Appl
44	45	26.3	84	1	US-08-452-592B-8	Sequence 8, Appl
45	45	26.3	285	1	US-08-410-540-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-469-486-56
; Sequence 56, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoeqersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-56

Query Match 85.4%; Score 146; DB 1; Length 202;
Best Local Similarity 80.6%; Pred. No. 1.4e-13;

; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,456A
; FILING DATE: 29-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-129-456A-36

Query Match 29.2%; Score 50; DB 1; Length 310;
Best Local Similarity 61.1%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 MDVLAQEVALLKEKQALQ 31
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Db 22 IEYLKQVALLKEKAILQ 39

RESULT 6

US-08-705-868-3
; Sequence 3, Application US/08705868
; Patent No. 5885798
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,868
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 498910
US-08-705-868-3

Query Match 29.2%; Score 50; DB 2; Length 310;
Best Local Similarity 61.1%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 MDVLAQEVALLKEKQALQ 31
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Db 22 IEYLKQVALLKEKAILQ 39

RESULT 7

US-09-123-615-3
; Sequence 3, Application US/09123615
; Patent No. 6090377
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,615
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,868
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0117 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 498910
US-09-123-615-3

Query Match 29.2%; Score 50; DB 3; Length 310;
Best Local Similarity 61.1%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 MDVLAQEVALLKEKQALQ 31
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Db 22 IEYLKQVALLKEKAILQ 39

RESULT 8

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US-08-360-821B-35
; Sequence 35, Application US/08360821B
; Patent No. 6228837
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; POLYPEPTIDE II: A Mediator Which Activates Host Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821B
; FILING DATE: 08-OCT-96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-360-821B-35

Query Match          29.2%; Score 50; DB 4; Length 310;
Best Local Similarity 61.1%; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

QY 14 MDVLAEQVALLKEKQALQ 31
DB 22 IEYKQVALLKEKAILQ 39

RESULT 9
US-08-928-213B-8
; Sequence 8, Application US/08928213B
; Patent No. 6238905
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles S.
; APPLICANT: Seville, Mark G.
; APPLICANT: Cull, Millard G.
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
; HOOLOENZYME
; NUMBER OF SEQUENCES: 195
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,213B
; FILING DATE: 12-Sep-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: ENZYCO-02550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-928-213B-8

Query Match          29.2%; Score 50; DB 4; Length 528;
Best Local Similarity 46.4%; Pred. No. 28;
Matches 13; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 8 EELKNRMDVLAEQVALLKEKQALQTVCL 35
DB 317 ERLRRSDALSLEVALLEAGRALAAEAL 344

RESULT 10
US-08-404-665-4
; Sequence 4, Application US/08404665
; Patent No. 5591583
; GENERAL INFORMATION:
; APPLICANT: Reid, Robert A.
; APPLICANT: Ackley, Rhonda L.
; APPLICANT: Hemperly, John J.
; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
; SEQUENCES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; COMPANY
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,665
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3341
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-404-665-4

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ADDRESSEE: Richard J. Rodrick. Becton Dickinson and

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:43:14 ; Search time 28.75 seconds
(without alignments)
166.853 Million cell updates/sec

Title: US-09-445-576A-37

Perfect score: 171

Sequence: 1 LVSKMPEELKRMNDVLAQEVALLKEKQALQTVCLK 36

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	85.4	180	AAW94264	H6FTN23 fusion pr
2	146	85.4	181	AAW94256	Human tetranectin
3	146	85.4	197	AAW94262	H6FTN123 fusion p
4	146	85.4	202	AAW60521	Human tetranectin.
5	146	85.4	202	AAW24034	Human EST encoded
6	146	85.4	228	AAW94261	CIH6FTN123 fusio
7	141	82.5	182	AAW60098	Sequence of chain
8	136	79.5	52	AAW94254	Tetranectin polype
9	136	79.5	73	AAW94270	H6Ftripa fusion p
10	128	74.9	49	AAW94255	Tetranectin polype

11	128	74.9	65	20	AAW94263	H6FTN12 fusion pr
12	124	72.5	69	20	AAW94271	H6Ftripb fusion p
13	124	72.5	145	20	AAW94266	H6Ftripb-UB fusio
14	124	72.5	330	20	AAW94267	H6FXScFV(C6A6)trip
15	124	72.5	331	20	AAW94268	H6FXtripBScFV(C6A6
16	124	72.5	592	20	AAW94269	H6FXScFV(C6A6)trip
17	82	48.0	59	21	AAW00261	Human secreted pro
18	72	42.1	197	21	AAW82526	protein encoded by
19	72	42.1	197	23	AAW82642	Human breast tumou
20	72	42.1	206	21	AAW66756	Membrane-bound pro
21	72	42.1	206	22	AAW29161	Human PKO polypt
22	72	42.1	206	22	AAW65279	Human PRO1345 (UNQ
23	72	42.1	206	23	AAE20465	Human tumour-assoc
24	61	35.7	1212	22	ABW71114	Drosophila melanog
25	58.5	34.2	137	23	ABP28176	Streptococcus poly
26	57	33.3	920	23	ABP25932	Streptococcus poly
27	54.5	31.9	1833	22	ABW71141	Drosophila melanog
28	54	31.6	739	22	ABB70356	Drosophila melanog
29	54	31.6	751	22	ABB32409	Peptide #5060 enco
30	54	31.6	751	22	ABB37862	Peptide #5368 enco
31	54	31.6	751	22	ABB23121	Protein #5120 enco
32	54	31.6	751	22	AAW58492	Human brain expres
33	54	31.6	751	22	AAW70992	Human bone marrow
34	54	31.6	751	22	AAW18634	Peptide #5068 enco
35	54	31.6	751	22	AAW31268	Peptide #5305 enco
36	54	31.6	751	23	AAW06199	Peptide #4881 enco
37	54	31.6	751	23	ABG40780	Human peptide enco
38	54	31.6	761	20	AAW28934	CEV14 gene product
39	54	31.6	2017	22	ABG06301	Novel human diagno
40	53.5	31.3	403	22	AAW98859	E. coli growth and
41	53	31.0	830	21	AAW96730	PRO539, a Costal-2
42	53	31.0	830	23	AAW86160	Human PRO539 polyp
43	53	31.0	895	23	ABW97536	Novel human protei
44	53	31.0	895	23	AAW86164	Human alpha T-cate
45	53	31.0	895	23	AAW86185	Mouse alpha T-cate

ALIGNMENTS

RESULT 1
AAW94264
ID AAW94264 standard; protein: 180 AA.
XX AAW94264;
XX AC
XX AC
XX AC
DT 26-APR-1999 (first entry)
XX H6FTN23 fusion protein sequence.

DE Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
KW transfection; imaging; tumour; human; tetranectin; H6FTN23.

XX Synthetic.
XX OS Homo sapiens.

XX WO9856906-A1.

XX 17-DEC-1998.

XX 11-JUN-1998; 98WO-DK00245.

XX 11-JUN-1997; 97DK-0000685.

XX (ETZE/) ETZERODT M.

PA (GRAV/) GRAVERSEN N J H.

PA (HOLT/) HOLTET T L.

PA (KAST/) KASTRUP J S.

XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;

PI Larsen IK, Nielsen BB, Thøgersen HC;

XX PN WO9856906-A1.
 XX PD 17-DEC-1998.
 XX PF 11-JUN-1998; 98WO-DK00245.
 XX PR 11-JUN-1997; 97DK-0000685.
 XX PA (ETZE/) ETZERODT M.
 XX PA (GRAV/) GRAVERSEN N J H.
 XX PA (HOLT/) HOLTET T L.
 XX PA (KAST/) KASTRUP J S.
 XX PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 XX PI Larsen IK, Nielsen BB, Thogersen HC;
 XX DR WPI; 1999-080897/07.
 XX PT New monomer polypeptide constructs for diagnosis and therapy -
 XX PT comprise a tetranectin trimerising structural element covalently
 XX PT linked to at least one heterologous moiety for providing functional
 XX PT activity
 XX PS Disclosure; Fig 6; 110pp; English.
 XX CC The invention relates to the design of trimeric polypeptides using
 XX CC polypeptide structural elements derived from the tetranectin protein
 XX CC family. The trimeric polypeptides constructed as a monomer polypeptide
 XX CC construct comprise at least one tetranectin trimerising structural
 XX CC element (TTSE) which is covalently linked to at least one heterologous
 XX CC moiety, the TTSE being capable of forming a stable complex with 2 other
 XX CC TTSEs, with the proviso that the heterologous moiety is different from
 XX CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 XX CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 XX CC conjugates with heterologous moieties such as a ligand binding
 XX CC structure, a toxin, a detectable label, an in situ activatable substance,
 XX CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 XX CC a photo cross-linking agent, or a group facilitating conjugation of the
 XX CC monomer polypeptide construct to a target. They can be used as vehicles
 XX CC for assembling antibody fragments into oligomeric or multivalent
 XX CC entities for generating chimeric artificial antibodies having
 XX CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 XX CC constructs can be used for targeted gene therapy involving selective
 XX CC delivery of the material for transfection or infection of the specific
 XX CC population of cells. They can also be used for delivering a substance to
 XX CC a cell or tissue or for delivering an imaging or toxin-conjugated
 XX CC antibody to a tumour. They can also be used for prevention or treating a
 XX CC disease or for diagnosis. The TTSE provides a stable structure which can
 XX CC act as a vehicle for a wide variety of conjugates. The present sequence
 XX CC represents a H6FXTN123 fusion protein sequence. The specification claims
 XX CC that the heterologous moiety to which the TTSEs of the invention are
 XX CC linked to is specifically different from the present fusion protein
 XX CC sequence.
 XX SQ Sequence 197 AA;
 Query Match 85.4%; Score 146; DB 20; Length 197;
 Best Local Similarity 80.6%; Pred. No. 3.2e-11;
 Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LVSSKMFEEELKRNMDVLAQVEALLKEQALQTVCLK 36
 ::::|||||:::|:|||||:::|||||:::|||||
 Db 33 VVNTKMFEEELKSRDLTLAQVEALLKEQALQTVCLK 68
 RESULT 4
 AAR60521
 ID AAR60521 standard; Protein; 202 AA.
 XX AC AAR60521;
 XX DT 22-MAR-1995 (first entry)

XX DE Human tetranectin.
 XX KW Serine protease; Factor-Xa; recognition site; tetranectin;
 KW fusion protein cleavage; protein folding; primer;
 KW polymerase chain reaction; amplification.
 XX OS Homo sapiens.
 XX PN WO9418227-A.
 XX PD 18-AUG-1994.
 XX PF 04-FEB-1994; 94WO-DK00054.
 XX PR 04-FEB-1993; 93DK-0000130.
 XX PR 05-FEB-1993; 93DK-0000139.
 XX PR 03-DEC-1993; 93WO-GH02492.
 XX PA (DENZ-) DENZYME APS.
 XX PI Etzerodt M, Holtet TL, Thogersen HC;
 XX DR WPI; 1994-279681/34.
 XX PT Refolding of polypeptide molecules - using a cyclic process
 XX PT involving denaturing and renaturing conditions to produce a
 XX PT correctly folded prod
 XX PS Disclosure; Page 151-52; 202pp; English.
 XX CC cDNA encoding human tetranectin (full sequence given in AAR60521) was
 XX CC PCR amplified using primers given in AA071274-75. Amplified cDNA was
 XX CC linked to a sequence encoding the factor-Xa cleavage site (given in
 XX CC AAR60503), subcloned in vector pT7H6 so that it was linked to a
 XX CC hexahistidine-encoding sequence and expressed in E. coli BL21. The
 XX CC fusion protein was purified on an N12+-activated NTA-agarose column.
 XX CC A cyclic procedure was used to obtain correctly folded recombinant
 XX CC protein.
 XX SQ Sequence 202 AA;
 Query Match 85.4%; Score 146; DB 15; Length 202;
 Best Local Similarity 80.6%; Pred. No. 3.3e-11;
 Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LVSSKMFEEELKRNMDVLAQVEALLKEQALQTVCLK 36
 ::::|||||:::|:|||||:::|||||:::|||||
 Db 38 VVNTKMFEEELKSRDLTLAQVEALLKEQALQTVCLK 73
 RESULT 5
 AAM24034
 ID AAM24034 standard; Protein; 202 AA.
 XX AC AAM24034;
 XX DT 12-OCT-2001 (first entry)
 XX DE Human EST encoded protein SEQ ID NO: 1559.
 XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX OS Homo sapiens.
 XX PN WO200154477-A2.
 XX PD 02-AUG-2001.
 XX PF 25-JAN-2001; 2001WO-US02687.

```

XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI: 2001-476164/51.
DR N-PSDB; AAH98693.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 20; Page 1069; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
XX Sequence 202 AA;
SQ
Query Match 85.4%; Score 146; DB 22; Length 202;
Best Local Similarity 80.6%; Pred. No. 3.3e-11;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 LVSSKMFEEKNMDVLAQEVALLKKEQALQTVCLK 36
DB 38 VVNTKMFEEKLSRLDTLAQEVALLKKEQALQTVCLK 73
RESULT 6
AAW94261
ID AAW94261 standard; protein; 228 AA.
XX
XX AAW94261;
XX
XX 26-APR-1999 (first entry)
XX
XX CIIH6FXTN123 fusion protein sequence.
DE
XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
KW transfection; imaging; tumour; human; tetranectin; CIIH6FXTN123.
XX
XX Homo sapiens.
OS
XX
XX WO9856906-A1.
PN
XX
XX 17-DEC-1998.
PD
XX
XX 11-JUN-1998; 98WO-DK00245.
PF
XX
XX 11-JUN-1997; 97DK-0000685.
PR
XX (ETZE/) ETZERODT M.
PA
XX (GRAV/) GRAVERSEN N J H.
PA (HOLT/) HOLTET T L.
PA (KAST/) KASTRUP J S.
XX
XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
PI Larsen IK, Nielsen BB, Thøgersen HC;
XX
XX WPI: 1999-080897/07.
DR

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XX New monomer polypeptide constructs for diagnosis and therapy -
PT comprise a tetranectin trimerising structural element covalently
PT linked to at least one heterologous moiety for providing functional
PT activity
XX
XX Disclosure; Fig 6; 110pp; English.
XX
XX The invention relates to the design of trimeric polypeptides using
CC polypeptide structural elements derived from the tetranectin protein
CC family. The trimeric polypeptides constructed as a monomer polypeptide
CC construct comprise at least one tetranectin trimerising structural
CC element (TTSE) which is covalently linked to at least one heterologous
CC moiety, the TTSE being capable of forming a stable complex with 2 other
CC TTSEs, with the proviso that the heterologous moiety is different from
CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
CC conjugates with heterologous moieties such as a ligand binding
CC structure, a toxin, a detectable label, an in situ activatable substance,
CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
CC a photo cross-linking agent, or a group facilitating conjugation of the
CC monomer polypeptide construct to a target. They can be used as vehicles
CC for assembling antibody fragments into oligomeric or multivalent
CC entities for generating chimeric artificial antibodies having
CC selected pharmacokinetic and/or pharmacodynamic properties. The
CC constructs can be used for targeted gene therapy involving selective
CC delivery of the material for transfection or infection of the specific
CC population of cells. They can also be used for delivering a substance to
CC a cell or tissue or for delivering an imaging or toxin-conjugated
CC antibody to a tumour. They can also be used for prevention or treating a
CC disease or for diagnosis. The TTSE provides a stable structure which can
CC act as a vehicle for a wide variety of conjugates. The present sequence
CC represents a CIIH6FXTN123 fusion protein sequence. The specification
CC claims that the heterologous moiety to which the TTSEs of the invention
CC are linked to is specifically different from the present fusion protein
CC sequence.
XX
XX Sequence 228 AA;
SQ
Query Match 85.4%; Score 146; DB 20; Length 228;
Best Local Similarity 80.6%; Pred. No. 3.8e-11;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 LVSSKMFEEKNMDVLAQEVALLKKEQALQTVCLK 36
DB 64 VVNTKMFEEKLSRLDTLAQEVALLKKEQALQTVCLK 99
RESULT 7
AAP60098
ID AAP60098 standard; protein; 182 AA.
XX
XX AAP60098;
XX
XX 27-JUN-1991 (first entry)
DT
XX
XX Sequence of chain of Tetranectin protein.
DE
XX Plasminogen activation; clot lysis; fibrinolysis; tissue growth;
KW tissue repair; haemostasis; neoplasia therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Disulfide-bond 50..60
FT Disulfide-bond 77..176
FT Disulfide-bond 152..168
FT Misc-difference 37 /label= M,V
XX
XX EP206400-A.
XX
XX 30-DEC-1986.
PD

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```

XX 10-JUN-1986; 86EP-0201005.
XX
XX 11-JUN-1985; 85NL-0001682.
XX
XX (NEDE ) NEDERLAND ORG TNO.
XX
XX Duhl Clemmensen I, Klufft C;
XX
XX WPI; 1986-340760/52.
XX
XX New Tetranectin protein - purified from human blood plasma by
XX e.g. affinity chromatography on a column with coupled kringle 4
XX of plasminogen
XX
XX Claim 9; Page 1a; 12pp; English.
XX
XX Tetranectin is comprised of four polypeptide chains having the
XX formula shown in AAP60098. Tetranectin stimulates and controls the
XX plasminogen activation resulting in a higher rate of clot lysis or
XX fibrinolysis, esp. in the presence of blood platelets and in the
XX presence of a complex fibrin clot from blood. It stimulates and
XX controls the plasminogen activation in the absence of fibrin but in
XX the presence of a cofactor such as polylysine.
XX
XX Sequence 182 AA;
XX
XX Query Match 82.5%; Score 141; DB 7; Length 182;
XX Best Local Similarity 77.8%; Pred. No. 1.3e-10;
XX Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 LVSSKMFEEELKRMVDVLAQEAVALLEKEQALQTVCLK 36
XX ::::|||||:::|||||:::|||||:::|||||:::|||||
XX Db 17 VVNTKMFEEELKSRDLTLAQEAXALLKEQALQTVCLK 52
XX
XX RESULT 8
XX AAW94254
XX ID AAW94254 standard; protein; 52 AA.
XX
XX AC AAW94254;
XX
XX DT 26-APR-1999 (first entry)
XX
XX DE Tetranectin polypeptide fragment (residues 1-52).
XX
XX KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
XX fusion protein; ligand binding structure; toxin; enzyme; cytokine;
XX artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
XX transfection; imaging; tumour; human; tetranectin.
XX
XX OS Homo sapiens.
XX
XX PN W09856906-A1.
XX
XX PD 17-DEC-1998.
XX
XX PF 11-JUN-1998; 98WO-DK00245.
XX
XX PR 11-JUN-1997; 97DK-0000685.
XX
XX (ETZE/) ETZERODT M.
XX (GRAV/) GRAVERSEN N J H.
XX (HOLT/) HOLTET T L.
XX (KAST/) KASTRUP J S.
XX
XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
XX Larsen IK, Nielsen BB, Thogersen HC;
XX
XX WPI; 1999-080897/07.
XX
XX New monomer polypeptide constructs for diagnosis and therapy -
XX comprise a tetranectin trimerising structural element covalently

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PT linked to at least one heterologous moiety for providing functional
PT activity
XX
XX Example 1; Page 59; 110pp; English.
XX
XX The invention relates to the design of trimeric polypeptides using
XX polypeptide structural elements derived from the tetranectin protein
XX family. The trimeric polypeptides constructed as a monomer polypeptide
XX construct comprise at least one tetranectin trimerising structural
XX element (TTSE) which is covalently linked to at least one heterologous
XX moiety, the TTSE being capable of forming a stable complex with 2 other
XX TTSEs, with the proviso that the heterologous moiety is different from
XX any of the fusion proteins CIIH6FTN123, H6FTN123, H6FTN12, H6FTN23
XX (AAW94261 to AAW94264). The TTSE can be used for the construction of
XX conjugates with heterologous moieties such as a ligand binding
XX structure, a toxin, a detectable label, an in situ activatable substance,
XX an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
XX a photo cross-linking agent, or a group facilitating conjugation of the
XX monomer polypeptide construct to a target. They can be used as vehicles
XX for assembling antibody fragments into oligomeric or multivalent
XX entities for generating chimeric artificial antibodies having the
XX preselected pharmacokinetic and/or pharmacodynamic properties. The
XX constructs can be used for targeted gene therapy involving selective
XX delivery of the material for transfection or infection of the specific
XX population of cells. They can also be used for delivering a substance to
XX a cell or tissue or for delivering an imaging or toxin-conjugated
XX antibody to a tumour. They can also be used for prevention or treating a
XX disease or for diagnosis. The TTSE provides a stable structure which can
XX act as a vehicle for a wide variety of conjugates. The present sequence
XX represents a human tetranectin polypeptide fragment. The encoding nucleic
XX acid sequence was amplified by PCR from the plasmid clone pT7H6FTN123.
XX This is used in the construction of E. coli expression vectors for the
XX production of trimerised chimeric fusion proteins.
XX
XX Sequence 52 AA;
XX
XX Query Match 79.5%; Score 136; DB 20; Length 52;
XX Best Local Similarity 77.8%; Pred. No. 1.4e-10;
XX Matches 28; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 LVSSKMFEEELKRMVDVLAQEAVALLEKEQALQTVCLK 36
XX ::::|||||:::|||||:::|||||:::|||||:::|||||
XX Db 17 VVNTKMFEEELKSRDLTLAQEAXALLKEQALQTVSLK 52
XX
XX RESULT 9
XX AAW94270
XX ID AAW94270 standard; protein; 73 AA.
XX
XX AC AAW94270;
XX
XX DT 26-APR-1999 (first entry)
XX
XX DE H6FTXtripa fusion protein sequence.
XX
XX KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
XX fusion protein; ligand binding structure; toxin; enzyme; cytokine;
XX artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
XX transfection; imaging; tumour; human; tetranectin.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN W09856906-A1.
XX
XX PD 17-DEC-1998.
XX
XX PF 11-JUN-1998; 98WO-DK00245.
XX
XX PR 11-JUN-1997; 97DK-0000685.
XX
XX (ETZE/) ETZERODT M.
XX (GRAV/) GRAVERSEN N J H.

```


KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; H6FXTN12.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX W09856906-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX 11-JUN-1998; 98WO-DK00245.
 PF
 XX 11-JUN-1997; 97DK-0000685.
 PR
 XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX
 XX WPI: 1999-080897/07.
 DR
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 XX Disclosure; Fig 8; 110pp; English.
 PS
 XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXTN12 fusion protein sequence. The specification claims
 CC that the heterologous moiety to which the TTSEs of the invention are
 CC linked to is specifically different from the present fusion protein
 CC sequence.
 XX
 SQ Sequence 65 AA;
 Query Match 74.9%; Score 128; DB 20; Length 65;
 Best Local Similarity 78.8%; Pred. No. 2e-09; Indels 0; Gaps 0;
 Matches 26; Conservative 6; Mismatches 1;
 Qy 1 LVSSKMFEEELKRNMDVLAQEVALLKEKQALQTV 33
 Db 33 VVNTKMFEEELKSLRLTLAQEVALLKEKQALQTV 65

RESULT 12

Query Match 72.5%; Score 124; DB 20; Length 69;
 Best Local Similarity 78.1%; Pred. No. 7.2e-09;

AAW94271
 ID AAW94271 standard; protein; 69 AA.
 XX
 AC AAW94271;
 XX
 DT 26-APR-1999 (first entry)
 DE
 DE H6FXTripb fusion protein sequence.
 XX
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX W09856906-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX 11-JUN-1998; 98WO-DK00245.
 PF
 XX 11-JUN-1997; 97DK-0000685.
 PR
 XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX
 XX WPI: 1999-080897/07.
 DR
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 XX Disclosure; Fig 4; 110pp; English.
 PS
 XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXTripb fusion protein sequence encoded by the plasmid
 CC pH6FXTripb.
 XX
 SQ Sequence 69 AA;

CC for assembling antibody fragments into oligomeric or multivalent:

CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXScFv(CEA6)trpB fusion protein sequence encoded by the
 CC plasmid pH6FXScFv(CEA6)trpB
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 72.5%; Score 124; DB 20; Length 330;
 Best Local Similarity 78.1%; Pred. No. 4.2e-08;
 Matches 25; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LVSSKMFELKRMMDVLAQEVALLKEQALQT 32
 ::::|||||:::|:| |||||:::|||||
 Db 297 VVNTKMFELKSRDLTLAQEVALLKEQALQT 328
 ::::|||||:::|:| |||||:::|||||
 RESULT 15
 AAW94268
 ID AAW94268 standard; protein; 331 AA.
 XX
 AC AAW94268;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE H6FXtripBscFv(CEA6) fusion protein sequence.
 XX
 KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; CEA6.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09856906-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-DK00245.
 XX
 PR 11-JUN-1997; 97DK-0000685.
 XX
 PA (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thøgersen HC;
 XX
 DR WPI; 1999-080897/07.
 XX
 PT New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Example 4; Fig 18; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from

CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXtripBscFv(CEA6) fusion protein sequence encoded by the
 CC plasmid pH6FXtripBscFv(CEA6)
 XX
 XX Sequence 331 AA;
 SQ
 Query Match 72.5%; Score 124; DB 20; Length 331;
 Best Local Similarity 78.1%; Pred. No. 4.2e-08;
 Matches 25; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LVSSKMFELKRMMDVLAQEVALLKEQALQT 32
 ::::|||||:::|:| |||||:::|||||
 Db 36 VVNTKMFELKSRDLTLAQEVALLKEQALQT 67
 ::::|||||:::|:| |||||:::|||||
 Search completed: April 15, 2003, 11:47:58
 Job time : 29.75 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	123	71.5	201	13	Q9DD4	Q9dd44 gallus galli	
2	84	48.8	196	11	Q9EPW4	Q9epw4 mus musculus	
3	79	45.9	197	6	Q28008	Q28008 bos taurus	
4	60	34.9	761	4	O14689	O14689 homo sapien	
5	60	34.9	794	17	Q8ZVH4	Q8zv44 pyrobaculum	
6	60	34.9	1978	4	O15154	O15154 homo sapien	
7	59	34.3	1583	12	Q90304	Q90304 bredda virus	
8	59	34.3	1979	4	Q95949	Q95949 homo sapien	
9	58	33.7	488	5	Q9W2K9	Q9w2k9 drosophila	
10	58	33.7	853	10	Q9LPE4	Q9lpe4 arabidopsis	
11	57.5	33.4	279	5	O00867	O00867 plasmodium	
12	57.5	33.4	309	16	Q8XLN6	Q8xln6 clostridium	
13	57	33.1	307	16	Q8ZL10	Q8zll0 salmonella	
14	57	33.1	307	16	Q8Z2L2	Q8z2l2 salmonella	
15	56	32.6	185	16	Q8R6C6	Q8r6c6 thermococcus	
16	55.5	32.3	1970	10	Q9LM53	Q9lm53 arabidopsis	

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AC Q9EPW4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C-type lectin superfamily 1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES129/SV;
RA Neame P.J., Grimm D.R.;
RT "Mouse homolog of human CLEC5F1, a cartilage derived C-type lectin.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR HMBL; AF317204; AAG48620.1; -
DR HSSP; P05452; 1HTN.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;

Query Match 48.8%; Score 84; DB 11; Length 196;
Best Local Similarity 58.6%; Pred. No. 0.0075;
Matches 17; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 8 ELKSRDLTLAQEVALLEKQALQTVCLK 36
DB 42 DDLKQVEKLWREVNALKEMQALQTVCLR 70

RESULT 3
Q28008
ID Q28008 PRELIMINARY; PRT; 197 AA.
AC Q28008;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE C-type lectin homolog precursor.
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CARILAGE;
RA Neame P.J., Boynton R.E.;
RT "C-type lectin homolog from bovine cartilage.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22298; AAC18614.1; -
DR HSSP; P05452; 1TN3.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 197 C-TYPE LECTIN HOMOLOG.
SQ SEQUENCE 197 AA; 22215 MW; AAC4280F41AC0F4 CRC64;

Query Match 45.9%; Score 79; DB 6; Length 197;
Best Local Similarity 57.1%; Pred. No. 0.032;
Matches 16; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 9 ELKSRDLTLAQEVALLEKQALQTVCLK 36
DB 43 DDLKQVEKLWREVNALKEMQALQTVCLR 70

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RESULT 4
O14689
ID O14689 PRELIMINARY; PRT; 761 AA.
AC O14689;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CEV14 (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98043615; PubMed=9373237;
RA Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;
RT "Fusion of the platelet-derived growth factor receptor beta to a novel
RT gene CEV14 in acute myelogenous leukemia after clonal evolution.";
RL Blood 90:4271-4277(1997).
DR EMBL; AF011368; AAB84386.1; -
DR NON_TER 1
SQ SEQUENCE 761 AA; 87160 MW; 75DD86243E9F0CF5 CRC64;

Query Match 34.9%; Score 60; DB 4; Length 761;
Best Local Similarity 44.1%; Pred. No. 30;
Matches 15; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 2 VNTKMFELKSRDLTLAQEVALLEK--QALQTV 33
DB 12 VNSNOFEELLQERDLKQVKRMEWKOQVMTTV 45

RESULT 5
Q8ZVH4
ID Q8ZVH4 PRELIMINARY; PRT; 794 AA.
AC Q8ZVH4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein PAE2280.
GN PAE2280.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009867; AAL64082.1; -
DR InterPro; IPR002106; AACRNA_ligaseII.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02463; SMC_N; 1.
DR DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 794 AA; 91123 MW; 530347055A96034C CRC64;

Query Match 34.9%; Score 60; DB 17; Length 794;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 7 FEELKSRDLTLAQEVALLEKQ 28
DB 205 FQGLKARLDLAGEINALKERE 226

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DE Golgi-associated microtubule-binding protein.
GN GMAP-210.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE=9207053; PubMed=10189370;
RA Infante C., Ramos-Morales F., Fedriani F., Bornens M., Rios R.M.;
RT "GMAP-210, a cis-Golgi network-associated protein, is a minus end
microtubule-binding protein.";
RL J. Cell Biol. 145:83-98(1999).
DR EMBL; Y12490; CAA73095.1; -.
SQ SEQUENCE 1979 AA; 227639 MW; 83E46777D34D360D CRC64;

Query Match 34.3%; Score 59; DB 4; Length 1979;
Best Local Similarity 44.1%; Pred. No. 1;er02;
Matches 15; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 2 VNTKMFEEELSRDLTLAGOEVALLKE--QOALQTV 33
||: ||||| | | | | | | | | | | | | | |
Db 1199 VNSHOFEEELQERDLKQOVKKMEWKKQVMTTV 1232

RESULT 9
Q9W2K9 PRELIMINARY; PRT; 488 AA.
AC Q9W2K9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE CG9415 protein.
GN XBP1 OR CG9415.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Murphy L., Muzny D.M., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

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RESULT 6
O15154 PRELIMINARY; PRT; 1978 AA.
AC O15154;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Trip230.
GN TRIP230.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97404344; PubMed=9256431;
RA Chang K.H., Chen Y., Chen T.T., Chou W.H., Chen P.L., Ma Y.T.,
RA Yang-Feng T.L., Leng L., Tsai M.J., O'Malley B.W., Lee W.H.;
RT "A thyroid hormone receptor coactivator negatively regulated by the
retinoblastoma protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9040-9045(1997).
DR EMBL; AF007217; AAD09135.1; -.
SQ SEQUENCE 1978 AA; 227514 MW; AACB4EB45C75FD7E CRC64;

Query Match 34.9%; Score 60; DB 4; Length 1978;
Best Local Similarity 44.1%; Pred. No. 79;
Matches 15; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 2 VNTKMFEEELSRDLTLAGOEVALLKE--QOALQTV 33
||: ||||| | | | | | | | | | | | | | |
Db 1199 VNSHOFEEELQERDLKQOVKKMEWKKQVMTTV 1232

RESULT 7
Q90304 PRELIMINARY; PRT; 1583 AA.
AC Q90304;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Peplomer protein.
OS Breda virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=46473;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094374; PubMed=9879765;
RA Duckmanton L.M., Tellier R., Liu P., Petric M.;
RT "Bovine torovirus: sequencing of the structural genes and expression
of the nucleocapsid protein of Breda virus.";
RL Virus Res. 58:83-96(1998).
DR EMBL; AF076621; AAD03840.1; -.
SQ SEQUENCE 1583 AA; 177785 MW; 0529C1293B38849C CRC64;

Query Match 34.3%; Score 59; DB 12; Length 1583;
Best Local Similarity 48.1%; Pred. No. 84;
Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 TKMFEEELSRDLTLAGOEVALLKEQOAL 30
||: ||||| | | | | | | | | | | | | | |
Db 1157 TKNFEEISSLTLGQQVDFQSOTSL 1183

RESULT 8
O95949 PRELIMINARY; PRT; 1979 AA.
AC O95949;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

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RA Svrlskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: AEO03453; AAF46681.1; -;
 DR HSP: P05412; 1FOS.
 DR FLYBase: FBgn0021872; Xbp1.
 DR InterPro: IPR004827; TF_BZIP.
 DR Pfam: PF00170; bZIP; 1.
 DR SMART: SM00338; BRLZ; 1.
 DR PROSITE: PS00036; BZIP_BASIC; 1.
 KW DNA-binding; Nuclear protein.
 SQ SEQUENCE 488 AA; 52359 MW; C05AD488DE40A59 CRC64;
 Query Match 33.7%; Score 58; DB 5; Length 488;
 Best Local Similarity 48.1%; Pred. No. 33;
 Matches 13; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 QY 9 ELKSRDLTLAQEVALLKEQALQTVCL 35
 DB 143 KLDSELLRLQELAEKQKQOQHNTRCI 169
 RESULT 10
 Q9LFE4
 ID Q9LFE4 PRELIMINARY; PRT; 853 AA.
 AC Q9LFE4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Hypothetical 96.2 kDa protein.
 GN F5E19.70.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
 RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL391147; CAC01837.1; -;
 DR InterPro: IPR002017; Spectrin.
 DR SMART: SM00150; SPEG; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 853 AA; 96207 MW; E87563A667F11AAD CRC64;
 Query Match 33.7%; Score 58; DB 10; Length 853;
 Best Local Similarity 48.5%; Pred. No. 59;
 Matches 16; Conservative 4; Mismatches 11; Indels 2; Gaps 1;
 QY 3 NTKMFEELKSRDLTLAQEV--ALLKEQALQTV 33
 DB 406 NEKEVEKLKSELETVEEKNRALKKEQDATSRV 438
 RESULT 11
 O00867
 ID O00867 PRELIMINARY; PRT; 279 AA.
 AC O00867;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Hypothetical 32.1 kDa protein.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB3;
 RX MEDLINE=92118046; PubMed=1731798;
 RA Guntaka R.V., Kandala J.C., Reddy V.D.;
 RT "Cloning and characterization of a highly conserved HMG-like protein
 (Pf16) gene from Plasmodium falciparum,";
 RL Biochem. Biophys. Res. Commun. 182:412-419(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB3;
 RA Nambiar A., Kandala J.C., Dolan S.A., Jensen J.J., Guntaka R.V.;
 RT "Molecular cloning and characterization of a cDNA for the highly
 conserved HMG-like protein (Pf16) gene of Plasmodium falciparum,";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U97128; AAB58115.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA; 32106 MW; B44E9E202191C432 CRC64;
 Query Match 33.4%; Score 57.5; DB 5; Length 279;
 Best Local Similarity 46.4%; Pred. No. 22;
 Matches 13; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 3 NTKMFEELKSRDLTLAQEVALLKEQQA 29
 DB 108 NTSNFENIKSTIESTNCDEIALLKDKDA 135

RESULT 12
 Q8XLN6
 ID Q8XLN6 PRELIMINARY; PRT; 309 AA.
 AC Q8XLN6;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Probable divalent cation transporter.
 GN CPE1005.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater,";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003189; BAB80711.1; -;
 DR InterPro: IPR02523; CorA.
 DR Pfam: PF01544; CorA; 1.
 KW Complete proteome.
 SQ SEQUENCE 309 AA; 36468 MW; 62C34557D95C8A1C CRC64;
 Query Match 33.4%; Score 57.5; DB 16; Length 309;
 Best Local Similarity 48.0%; Pred. No. 24;
 Matches 12; Conservative 10; Mismatches 2; Indels 1; Gaps 1;

QY 2 VNTKMFEELKSRDLTLAQEVALLKE 26
 DB 212 INSKI-EKLITSLDTLSOELAIVRE 235

RESULT 13
 Q8ZLL0
 ID Q8ZLL0 PRELIMINARY; PRT; 307 AA.

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AC Q82L10;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Transcriptional activator (LysR family).
GN DSCC OR STM3800.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=2153498; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008877; AAU22660.1; -
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 307 AA; 35027 MW; 092B720ABB2F828C CRC64;

Query Match 33.1%; Score 57; DB 16; Length 307;
Best Local Similarity 44.8%; Pred. NO. 28;
Matches 13; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 5 KNFEELKSRLDTLAQEVALLKEQQALQIV 33
Db 77 RVFWALKSSLDTLNQEILDKNQELSGTL 105

RESULT 14
Q82L2L2
AC Q82L2L2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE D-serine deaminase activator.
GN STY3979.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627280; CAD03193.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH_1; 1.

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DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 307 AA; 35057 MW; 093B234FFB2F828C CRC64;

Query Match 33.1%; Score 57; DB 16; Length 307;
Best Local Similarity 44.8%; Pred. NO. 28;
Matches 13; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 5 KNFEELKSRLDTLAQEVALLKEQQALQIV 33
Db 77 RVFWALKSSLDTLNQEILDKNQELSGTL 105

RESULT 15
Q8R8C6
AC Q8R8C6;
ID Q8R8C6 PRELIMINARY; PRT; 185 AA.
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE2080.
GN TTE2080.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013156; AAM25253.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 185 AA; 21113 MW; 7EF54897A39F8266 CRC64;

Query Match 32.6%; Score 56; DB 16; Length 185;
Best Local Similarity 42.3%; Pred. NO. 22;
Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 3 NTKMFEELKSRLDTLAQEVALLKEQQ 28
Db 87 NSKLQELKNPDSIMQSIDLLERQ 112

Search completed: April 15, 2003, 11:50:09
Job time : 25.5 secs

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GenCore version 5.1.4_p5_4578
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OW protein - protein search, using sw model

Run on: April 15, 2003, 11:44:09 ; Search time 6.5 Seconds
(without alignments)
229.715 Million cell updates/sec

Title: US-09-445-576A-36

Perfect score: 172

Sequence: 1 VVNTKMFELKSLDLTLAQEVALLKEQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	202	1 TETN_HUMAN	P05452 homo sapien
2	146	84.9	202	1 TETN_MOUSE	P43025 mus musculu
3	84	48.8	166	1 TETN_CARSP	P26258 carcharhinu
4	75	43.6	197	1 CLF1_HUMAN	O75596 homo sapien
5	57	33.1	311	1 DSDC_ECOLI	P46068 escherichia
6	56	32.6	425	1 SYS_BACHD	O9Kgn4 bacillus ha
7	55.5	32.3	252	1 YRY2_CABEL	Q10006 caenorhabdi
8	53	30.8	197	1 YD99_METJA	Q58794 methanococc
9	52.5	30.5	275	1 RM13_YEAST	Q02204 saccharomyc
10	52	30.2	355	1 RF1_CAMJF	Q9pm63 campylobact
11	52	30.2	524	1 YE33_SYNY3	P74217 synechocyst
12	52	30.2	3433	1 UTRC_HUMAN	P46939 homo sapien
13	51.5	29.9	4367	1 DYHC_NEUCR	P45443 neurospora
14	51	29.7	351	1 ATP4_HUMAN	P18848 homo sapien
15	51	29.7	895	1 RA50_THEVO	P38302 thermoplasm
16	51	29.7	1010	1 ALA3_CHICK	P24798 gallus gall
17	50.5	29.4	679	1 YKR9_YEAST	P34237 saccharomyc
18	50	29.1	224	1 YJ7_YEAST	P47056 saccharomyc
19	50	29.1	249	1 CYSE_SYNY3	P74089 synechocyst
20	50	29.1	260	1 TNF5_FELCA	Q97605 felis silve
21	50	29.1	504	1 MYOC_HUMAN	Q99972 homo sapien
22	50	29.1	877	1 SYA_SYNY3	P74423 synechocyst
23	50	29.1	991	1 Y419_HUMAN	O43303 homo sapien
24	49.5	28.8	220	1 VHCW_BACSU	P54607 bacillus su
25	49.5	28.8	893	1 GEFH_HUMAN	Q92974 homo sapien
26	49.5	28.8	1032	1 KINN_HUMAN	Q12840 homo sapien
27	49.5	28.8	2222	1 DPOE_YEAST	P21951 saccharomyc
28	49	28.5	71	1 RL29_RICCN	Q92gx4 rickettsia
29	49	28.5	71	1 RL29_RICPR	Q92c13 rickettsia
30	49	28.5	311	1 LYSR_ECOLI	P03030 escherichia
31	49	28.5	425	1 SYS_BACSU	P37464 bacillus su
32	49	28.5	451	1 V110_FOWPV	P36700 fowlpox vir
33	49	28.5	541	1 NFL_RAT	P19527 rattus norv

RESULT 1									
TETN_HUMAN	49	28.5	542	1	NFL_MOUSE	P08551 mus musculu			
ID	AC	P05452;	49	28.5	544	1 NFL_XENLA			
DT	01-NOV-1988	(Rel. 09, Created)	49	28.5	548	1 NFL_PIG			
DT	01-APR-1993	(Rel. 25, Last sequence update)	49	28.5	554	1 NFL_BOVIN			
DT	15-JUN-2002	(Rel. 41, Last annotation update)	49	28.5	554	1 NFL_TAUROS			
DE	Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).	TNA.	49	28.5	595	1 PFR2_TRYBB			
GN	Homo sapiens (Human).	OS	49	28.5	1627	1 ADP1_MYCPN			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	49	28.5	3106	1 LMA2_MOUSE			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	OC	49	28.5	886	1 RA50_ARCFU			
OX	NCBI_TaxID=9606;	OX	48.5	28.2	1260	1 MY5B_HUMAN			
[1]	SEQUENCE FROM N.A.	RP	48.5	28.2	2022	1 ANT1_ONCVO			
RP	TISSUE=Placenta;	RP	48	27.9	102	1 YNI6_YEAST			
RC	MEDLINE=92365345; PubMed=1354271;	RC	48	27.9	110	1 YHBJ_ACTAC			
RX	Wever U.M., Albrechtsen R.;	RX							
RA	"tetranectin, a plasminogen kringle 4-binding protein. Cloning and	RA							
RT	gene expression pattern in human colon cancer.";	RT							
RL	Lab. Invest. 67:253-262(1992).	RL							
RN	[2]	RN							
RP	SEQUENCE FROM N.A.	RP							
RX	MEDLINE=92380263; PubMed=1511740;	RX							
RA	Berglund L., Petersen T.E.;	RA							
RT	"The gene structure of tetranectin, a plasminogen binding protein.";	RT							
RL	FEBS Lett. 309:15-19(1992).	RL							
RN	[3]	RN							
RP	SEQUENCE FROM N.A.	RP							
RC	TISSUE=Lung;	RC							
RA	Strausberg R.;	RA							
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.	RL							
RN	[4]	RN							
RP	SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58.	RP							
RX	MEDLINE=88107595; PubMed=3427041;	RX							
RA	Pohlendorff J., Clemmensen I., Magnusson S.;	RA							
RT	"Primary structure of tetranectin, a plasminogen kringle 4 binding	RT							
RT	plasma protein: homology with asialoglycoprotein receptors and	RT							
RL	cartilage proteoglycan core protein.";	RL							
RL	Biochemistry 26:6757-6764(1987).	RL							
RN	[5]	RN							
RP	SEQUENCE OF 1-36 FROM N.A.	RP							
RC	TISSUE=Placenta;	RC							
RA	Sorensen C.B., Berglund L., Petersen T.E.;	RA							
RT	"Cloning and mapping of the murine tetranectin gene.";	RT							
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBDJ databases.	RL							
RN	[6]	RN							
RP	PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106.	RP							
RC	TISSUE=Plasma;	RC							
RX	MEDLINE=20080486; PubMed=10614823;	RX							
RA	Jacquinod M., Holtet T.L., Etzerodt M., Clemmensen I., Thøgersen H.C.,	RA							
RA	Roepstorff P.;	RA							
RT	"Mass spectrometric characterisation of post-translational	RT							
RT	modification and genetic variation in human tetranectin.";	RT							
RL	Biol. Chem. 380:1307-1314(1999).	RL							
RN	[7]	RN							

```

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=97398360; PubMed=9256258;
RA Nielsen B.B., Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H.,
RA Etzerodt M., Thøgersen H.C., Larsen I.K.;
RT "Crystal structure of tetranectin, a trimeric plasminogen-binding
RT protein with an alpha-helical coiled coil.";
RL FEBS Lett. 412:388-396(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 66-202.
RX MEDLINE=98437604; PubMed=9757090;
RA Kastrup J.S., Nielsen B.B., Rasmussen H., Holtet T.L., Graversen J.H.,
RA Etzerodt M., Thøgersen H.C., Larsen I.K.;
RT "Structure of the C-type lectin carbohydrate recognition domain of
RT human tetranectin.";
RL Acta Crystallogr. D 54:757-766(1998).
CC -!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules destined for
CC exocytosis.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=20535.8; MW_ERR=2.4; METHOD=Electrospray;
CC RANGE=22-202.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC
CC -----
CC EMBL; X70910; CAA50265.1; -.
CC DR EMBL; X70911; CAA50265.1; JOINED.
CC DR EMBL; X70912; CAA50265.1; JOINED.
CC DR EMBL; X64559; CAA45860.1; -.
CC DR EMBL; BC011024; AAHL1024.1; -.
CC DR EMBL; X98121; CAA66803.1; -.
CC DR PIR; A29747; A29747.
CC DR PIR; S19865; S19865.
CC DR PIR; S24126; S24126.
CC DR PDB; 1HTN; 03-DEC-97.
CC DR PDB; ITN3; 06-MAY-98.
CC DR Genew; HGNC:11891; TNA.
CC MIM; 187520; -.
CC DR InterPro; IPR001304; Lectin_C.
CC DR Pfam; PF00059; Lectin_c; 1.
CC DR SMART; SM00034; CLECT; 1.
CC DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC KW Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
CC FT SIGNAL 1 21
CC FT CHAIN 22 202 TETRALECTIN.
CC FT DOMAIN 77 198 C-TYPE LECTIN.
CC FT DISULFID 71 81
CC FT DISULFID 98 197
CC FT DISULFID 173 189
CC FT CARBOHYD 25 25
CC FT VARIANT 55 55
CC FT A -> S.
CC FT /FTID=VAR_004189.
CC FT V -> M.
CC FT /FTID=VAR_004190.
CC FT S -> G.
CC FT /FTID=VAR_012318.
CC FT /FTID=VAR_012318.
CC SQ SEQUENCE 202 AA; 22567 MW; 2B0DCB5DF22E1AB8 CRC64;
Query Match 100.0%; Score 172; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VVNTKMFELSRDLTQAQEVALLKEQALQTVCLK 36
DB 38 VVNTKMFELSRDLTQAQEVALLKEQALQTVCLK 73

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RESULT 2

```

TETN_MOUSE
ID TETN_MOUSE STANDARD: PRT; 202 AA.
AC P43025;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
GN TNA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Lung;
RX MEDLINE=95137396; PubMed=7835708;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of a cDNA encoding murine tetranectin.";
RL Gene 152:243-245(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=96116955; PubMed=8563165;
RA Ibaraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.;
RT "Mouse tetranectin: cDNA sequence, tissue-specific expression, and
RT chromosomal mapping.";
RL Mamm. Genome 5:693-696(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=98072445; PubMed=9409787;
RA Soerensen C.B., Berglund L., Petersen T.E.;
RT "Cloning of the murine tetranectin gene and 5'-flanking region.";
RL Gene 201:199-202(1997).
CC -!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
CC 4. May be involved in the packaging of molecules destined for
CC exocytosis (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC
CC -----
CC EMBL; X79199; CAA55791.1; -.
CC DR EMBL; U08595; AAA96811.1; -.
CC DR EMBL; X98122; CAA66804.1; -.
CC DR HSSP; P05452; ITN3.
CC DR MGD; MGI:104540; Tna.
CC DR InterPro; IPR001304; Lectin_C.
CC DR Pfam; PF00059; Lectin_c; 1.
CC DR SMART; SM00034; CLECT; 1.
CC DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC KW Lectin; Plasma; Signal.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 202 TETRALECTIN.
CC FT DOMAIN 77 198 C-TYPE LECTIN.
CC FT DISULFID 71 81 BY SIMILARITY.
CC FT DISULFID 98 197 BY SIMILARITY.
CC FT DISULFID 173 189 BY SIMILARITY.
CC FT CONFLICT 19 20 LT -> VI (IN REF. 2).
CC FT CONFLICT 84 84 A -> T (IN REF. 2).

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FT CONFLICT 180 180 A -> R (IN REF. 2).
FT CONFLICT 188 188 R -> Q (IN REF. 2).
SQ SEQUENCE 202 AA; 2257 MW; 639E7334D58EB04E CRC64;

Query Match 84.9%; Score 146; DB 1; Length 202;
Best Local Similarity 80.6%; Pred. No. 3.le-11;
Matches 29; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVNTKMFELSRDLTAEVALLKEQALQTVCLK 36
:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 38 LVSSKMFELNRMDVLAQEVALLKEQALQTVCLK 73

RESULT 3
TETN_CARSP
ID TETN_CARSP STANDARD; PRT; 166 AA.
AC P26258;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tetranectin-like protein.
OS Carcharhinus springeri (Reef shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Carcharhinidae; Carcharhinus.
OX NCBI_TaxID=7809;
RN [1]
RP SEQUENCE.
RC TISSUE=Neural arch cartilage;
RX MEDLINE=93284081; PubMed=1304877;
RA Neame P.J., Young C.N., Treep J.T.;
RT "Primary structure of a protein isolated from reef shark
(Carcharhinus springeri) cartilage that is similar to the mammalian
C-type lectin homolog, tetranectin."
RL Protein Sci. 1:161-168(1992).
CC -! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
PIR: A37289; A37289.
DR HSSP; P05452; IHTN.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW LECTIN; Cartilage.
FT DOMAIN 43 161 C-TYPE LECTIN.
FT DISULFID 37 47
FT DISULFID 64 160
FT DISULFID 136 152
SQ SEQUENCE 166 AA; 18432 MW; 53EF812DEA5C6119 CRC64;

Query Match 48.8%; Score 84; DB 1; Length 166;
Best Local Similarity 58.6%; Pred. No. 0.0012;
Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 8 BELKSRDLTAEVALLKEQALQTVCLK 36
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 11 DDLRNEIDKLWRENSLKEMQALQTVCLK 39

RESULT 4
CLF1_HUMAN
ID CLF1_HUMAN STANDARD; PRT; 197 AA.
AC O75596;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-type lectin superfamily member 1 precursor (cartilage-derived C-type
lectin).
GN CLECSF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99453719; PubMed=10524194;
RA Neame P.J., Tapp H., Grimm D.R.;
RT "The cartilage-derived, C-type lectin (CLECSF1): structure of the gene
and chromosomal location."
RL Biochim. Biophys. Acta 1446:193-202(1999).
CC -! TISSUE SPECIFICITY: Restricted to cartilage.
CC -! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC
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CC -----
CC EMBL; AF077345; AAD12542.1;
CC EMBL; AF077344; AAD12542.1; JOINED.
CC HSSP; P05452; IHTN.
CC Genew; HGNC:2052; CLECSF1.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW LECTIN; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.
FT DOMAIN 74 192 C-TYPE LECTIN.
FT DISULFID 68 78 BY SIMILARITY.
FT DISULFID 95 191 BY SIMILARITY.
FT DISULFID 167 183 BY SIMILARITY.
SQ SEQUENCE 197 AA; 22332 MW; BB924DBDB7729A4 CRC64;

Query Match 43.6%; Score 75; DB 1; Length 197;
Best Local Similarity 57.1%; Pred. No. 0.019;
Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 9 ELKSRDLTAEVALLKEQALQTVCLK 36
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 43 DLKTOIKLWTEVNAKKEIQALQTVCLR 70

RESULT 5
DSDC_ECOLI
ID DSDC_ECOLI STANDARD; PRT; 311 AA.
AC P46068; P77443;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE D-serine deaminase activator.
GN DSDC OR B2364.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;

RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC STRAIN=K12;
RX MEDLINE=96062227; PubMed=7592420;
RA Noerregaard-Madsen M., McFall E., Valentin-Hansen P.;
RT "Organization and transcriptional regulation of the Escherichia coli
K-12 D-serine tolerance locus."
RL J. Bacteriol. 177:6456-6461(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
MAU B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itah T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsushashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubramam S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
RA "Construction of a contiguous 874-kb sequence of the *Escherichia coli*
K-12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features";
RL DNA Res. 4:91-113(1997).
RN [4]
RP SEQUENCE OF 1-53 FROM N.A.
RC STRAIN=K12;
RX Brannigan J.A.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REGULATES THE EXPRESSION OF THE DSD OPERON FOR
CC D-SERINE DEAMINASE (DSDA).
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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CC -----
CC EMBL: X91821; CAA62931.1; -;
CC EMBL: AE000324; AAC75423.1; -;
CC EMBL: D90867; BAA16232.1; -;
CC EMBL: D90866; BAA16224.1; -;
CC EMBL: X86379; -; NOT_ANNOTATED_CDS.
CC EcoGene: EG13161; dsdC.
CC InterPro: IPR000847; HTH_LysR.
CC Pfam: PF00126; HTH_1; 1.
CC Pfam: PF03466; LysR_substrate; 1.
CC PRINTS: PR00039; HTHLYSR.
CC PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
KW Transcription regulation; DNA-binding; Activator; Complete proteome.
FT DNA_BIND 32 51 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 159 159 A -> R (IN REF. 1).
SQ SEQUENCE 311 AA; 35332 MW; 0335B060CF5DB3BB CRC64;

Query Match 33.1%; Score 57; DB 1; Length 311;
Best Local Similarity 41.9%; Pred. No. 5;
Matches 13; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 5 KMFEEKSLRLDTLQAEVALLKEQALQVCL 35
::: ||| |||| |:: |:: |:: |
DB 77 RVYWKSLSLDTLNQELDKNGELSGTLTL 107
::: ||| |||| |:: |:: |:: |

RESULT 6
ID SYS_BACHD STANDARD; PRT; 425 AA.
AC O9KGA;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerrS).
GN SERS OR BH0024.
OS *Bacillus halodurans*.
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
halodurans and genomic sequence comparison with *Bacillus subtilis*.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
CC + L-seryl-tRNA(Ser).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: AP001507; BAB03743.1; -;
CC HSP: P34945; 1SER.
CC InterPro: IPR002106; AALRNA_ligaseII.
CC InterPro: IPR002314; tRNA-synt_2b.
CC InterPro: IPR002317; tRNA-synt_ser.
CC Pfam: PF00587; tRNA-synt_2b; 1.
CC Pfam: PF02403; Seryl_tRNA_N; 1.
CC PRINTS: PR00981; TRNASYNTHSER.
CC TIGRFAMs: TIGR00414; serS; 1.
CC PROSITE: PS50862; AA_TRNA_LIGASE_II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 425 AA; 48541 MW; DB4F2EDA0EED676 CRC64;

Query Match 32.6%; Score 56; DB 1; Length 425;
Best Local Similarity 57.1%; Pred. No. 9.1;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 8 EELKSLRLDTLQAEVALLKEQ 28
||||| : |||| |::
DB 46 EELKSLRRNOVSQEAQLKREK 66
||||| : |||| |::

RESULT 7
ID YRY2_CAEEL STANDARD; PRT; 252 AA.
AC Q10006;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 29.4 kDa protein T15H9.2 in chromosome II.
GN T15H9.2.
OS *Caenorhabditis elegans*.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
CC Rhabditidae; Peloderinae; *Caenorhabditis*.
CC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gardner A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: 247356; CAA87415.1; -
DR WormPep; T15H9.2; CE01665.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29376 MW; 55AB2BA3F29414D2 CRC64;

Query Match 32.3%; Score 55.5; DB 1; Length 252;
Best Local Similarity 51.9%; Pred. No. 6.2;
Matches 14; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Oy 8 BELKSRDLTQAEVALLKEQO-ALQTV 33
   I::I::I I I::I::I I::I::I
Db 121 EQLKSQSLRDLSSVAILKSOQMAVKS 147

RESULT 8
YD99_METJA STANDARD; PRT; 197 AA.
AC Q58794;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein MJI399.
GN MJI399.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervaeke A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbaugh R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0200 FAMILY.
CC -----
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CC -----
DR EMBL: U67580; AAB99408.1; -
DR TIGR; MJI399; -
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 8 15 ATP (BY SIMILARITY).
SQ SEQUENCE 197 AA; 22630 MW; A440F8259920F873 CRC64;

Query Match 30.8%; Score 53; DB 1; Length 197;
Best Local Similarity 47.6%; Pred. No. 9.8;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRDLTQAEV 21
   I::I::I I::I::I I::I::I
Db 159 VVNEKSFEDCLNLDNLIQEI 179

RESULT 9
RM13_YEAST STANDARD; PRT; 275 AA.
ID RM13_YEAST
AC Q02204;

or send an email to license@isb-sib.ch).
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 60S ribosomal protein L13, mitochondrial precursor (YmL13).
GN MRPL13 OR YKR006C OR YK105.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93070612; PubMed=1441752;
RA Duesterhoeft A., Philippsen P.;
RT "DNA sequencing and analysis of a 24.7 kb segment encompassing
RT centromere CENII of Saccharomyces cerevisiae reveals nine previously
RT unknown open reading frames."
RL Yeast 8:749-759(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=07173;
RA Grohmann L., Kitakawa M., Isono K., Goldschmidt-Reisin S.,
RA Graack H.-R.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 87-120.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
CC -1- FUNCTION: COMPONENT OF THE LARGE SUBUNIT OF MITOCHONDRIAL
CC RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -----
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CC -----
DR EMBL: X65124; CAA46246.1; -
DR EMBL: X73673; CAA52022.1; -
DR EMBL: Z28231; CAA82076.1; -
DR PIR: S25816; S25816.
DR PIR: S17262; S17262.
DR SGD: S0001714; MRPL13.
KW Ribosomal protein; Mitochondrion; Transit peptide.
FT TRANSIT 1 86 MITOCHONDRION.
FT CHAIN 87 275 60S RIBOSOMAL PROTEIN L13.
FT CONFLICT 119 119 A -> S (IN REF. 2).
SQ SEQUENCE 275 AA; 31526 MW; 41F26BAA236E8826 CRC64;

Query Match 30.5%; Score 52.5; DB 1; Length 275;
Best Local Similarity 37.1%; Pred. No. 16;
Matches 13; Conservative 10; Mismatches 9; Indels 3; Gaps 1;

Oy 1 VVNTKMFELKSRDLTQAEVALLKE---QQAALQT 32
   I::I::I I::I::I I::I::I I::I::I
Db 237 VVNDVTSKEQSKYDVTIMKEIQKLEDDATRKALET 271

RESULT 10
RFL_CAMJE STANDARD; PRT; 355 AA.
ID RFL_CAMJE
AC Q9PM63;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptide chain release factor 1 (RF-1).

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GN PRFA OR CJ1612.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OC NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCCT 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagels K., Karlyshev A.V., Moulle S., Fallan M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 CC -1- FUNCTION: Peptide chain release factor 1 directs the termination
 CC of translation in response to the peptide chain termination codons
 CC UAG and UAA (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
 CC FACTORS FAMILY.
 CC -----
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 CC -----
 DR EMBL: AL139079; CAB73600.1; -
 DR InterPro: IPR005139; PCRF.
 DR InterPro: IPR000352; Pep_rel_factor_1.
 DR InterPro: IPR004373; Prfa.
 DR Pfam: PF00472; RF-1; 1.
 DR Pfam: PF03462; PCRF; 1.
 DR TIGRFAMs: TIGR000019; prfa; 1.
 DR PROSITE: PS00745; RF_PROK_1; 1.
 DR Protein biosynthesis: Complete proteome.
 KW SEQUENCE 355 AA; 39943 MW; 547F0202CB20B1B3 CRC64;
 SQ
 Query Match 30.2%; Score 52; DB 1; Length 355;
 Best Local Similarity 36.8%; Pred. No. 24;
 Matches 14; Conservative 7; Mismatches 11; Indels 6; Gaps 1;
 QY 5 KMFEELKSRIDT-----LAQEVALLKEQALQTVCLK 36
 DB 11 KRFEELNLSLSSDILNDISKMTLSKEQKNLEPIVLK 48
 RESULT 11
 YE33_SYNY3
 ID YE33_SYNY3 STANDARD; PRT; 524 AA.
 AC P74217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein sll1433.
 GN SLL1433.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -1- SIMILARITY: BELONGS TO THE UPF0031 FAMILY.
 CC -----
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 CC -----
 DR EMBL: D90913; BAA18311.1; -
 DR InterPro: IPR000631; UPF0031.
 DR InterPro: IPR004443; Yjef_Nterm.
 DR Pfam: PF01256; UPF0031; 1.
 DR TIGRFAMs: TIGR00196; Yjef_cterm; 1.
 DR TIGRFAMs: TIGR00197; Yjef_nterm; 1.
 DR PROSITE: PS01049; UPF0031_1; 1.
 DR PROSITE: PS01050; UPF0031_2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 524 AA; 55225 MW; 7E152799004133D7 CRC64;
 Query Match 30.2%; Score 52; DB 1; Length 524;
 Best Local Similarity 40.6%; Pred. No. 35;
 Matches 13; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 QY 1 VVNTKMFELKSRIDTLAQEVALLKEQALQ 32
 DB 11 VVSAQMGEIENWLFQTQGMFVAALMEKALQ 42
 RESULT 12
 UTRO_HUMAN
 ID UTRO_HUMAN STANDARD; PRT; 3433 AA.
 AC P46939;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Utrophin (Dystrophin-related protein 1) (DRP1) (DRP).
 GN UTRN OR DMDL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93096045; PubMed=1461283;
 RA Tinsley J.M., Blake D.J., Roche A., Fairbrother U., Riss J.,
 RA Byth B.C., Knight A.E., Kendrick-Jones J., Suthers G.K., Love D.R.,
 RA Edwards Y.H., Davies K.E.;
 RT "Primary structure of dystrophin-related protein.";
 RL Nature 360:591-593(1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 144-261.
 RX MEDLINE=99141377; PubMed=9887274;
 RA Keep N.H., Norwood F.L.M., Moores C.A., Winder S.J.,
 RA Kendrick-Jones J.;
 RT "The 2.0-A structure of the second calponin homology domain from the
 RT actin-binding region of the dystrophin homologue utrophin.";
 RL J. Mol. Biol. 285:1257-1264(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 31-256.
 RX MEDLINE=20113481; PubMed=10647184;
 RA Keep N.H., Winder S.J., Moores C.A., Walke S., Norwood F.L.M.,
 RA Kendrick-Jones J.;
 RT "Crystal structure of the actin-binding region of utrophin reveals a
 RT head-to-tail dimer.";
 RL Structure 7:1539-1546(1999).
 CC -1- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
 CC PLASMA MEMBRANE (BY SIMILARITY TO DYSTROPHIN).
 CC -1- SUBCELLULAR LOCATION: NEUROMUSCULAR JUNCTION.

CC -!- TISSUE SPECIFICITY: MUSCLE.
 CC -!- SIMILARITY: STRONG, TO DYSTROPHIN.
 CC -!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
 CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
 CC ABP-120, ABP-180, OR BETA-FODRIN).
 CC -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 WW DOMAIN.
 CC -!- SIMILARITY: CONTAINS 20 SPECTRIN REPEATS.
 CC -!- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
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 DR EMBL; X69086; CAA48829.1; -;
 DR PIR; S28381; S28381.
 DR PDB; 1BHD; 16-FEB-99.
 DR PDB; 1OAG; 01-JAN-00.
 DR Genew; HGNC:12635; UTRN.
 DR MIM; 128240; -;
 DR InterPro; IPR001589; Actbind_actnin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR002017; Spectrin.
 DR InterPro; IPR003122; TarH.
 DR InterPro; IPR002349; WW_Rsp5_WWP.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR InterPro; IPR000433; Znf_22.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00397; WW; 1.
 DR Pfam; PF00435; spectrin; 19.
 DR Pfam; PF00569; ZF; 1.
 DR PRINTS; PR00403; WWDOMAIN.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00150; SPEC; 18.
 DR SMART; SM00319; TarH; 1.
 DR SMART; SM00456; WW; 1.
 DR SMART; SM00291; Znf_22; 1.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 DR PROSITE; PS00020; WW_DOMAIN_2; 1.
 DR PROSITE; PS01357; ZF_22_1; 1.
 DR PROSITE; PS0135; ZF_22_2; 1.
 KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
 KW Repeat; 3D-structure; Zinc-finger.
 KW DOMAIN 1 246 ACTIN-BINDING.
 FT DOMAIN 31 135
 FT DOMAIN 150 252
 FT REPEAT 253 308 SPECTRIN 1.
 FT REPEAT 309 417 SPECTRIN 2.
 FT REPEAT 418 526 SPECTRIN 3.
 FT REPEAT 541 637 SPECTRIN 4.
 FT REPEAT 687 798 SPECTRIN 5.
 FT REPEAT 803 902 SPECTRIN 6.
 FT REPEAT 1016 1083 SPECTRIN 7.
 FT REPEAT 1125 1230 SPECTRIN 8.
 FT REPEAT 1248 1334 SPECTRIN 9.
 FT REPEAT 1432 1541 SPECTRIN 10.
 FT REPEAT 1544 1649 SPECTRIN 11.
 FT REPEAT 1652 1753 SPECTRIN 12.
 FT REPEAT 1910 1968 SPECTRIN 13.
 FT REPEAT 1976 2081 SPECTRIN 14.
 FT REPEAT 2258 2333 SPECTRIN 15.
 FT REPEAT 2399 2440 SPECTRIN 16.
 FT REPEAT 2443 2556 SPECTRIN 17.
 FT REPEAT 2559 2636 SPECTRIN 18.
 FT REPEAT 2658 2688 SPECTRIN 19.
 FT REPEAT 2691 2797 SPECTRIN 20.

FT DOMAIN 2812 2845 WW.
 FT ZN_FING 3064 3111 Z2-TYPE.
 SQ SEQUENCE 3433 AA; 394488 MW; EAE8DB409F858E5B CRC64;
 Query Match 30.2%; Score 52; DB 1; Length 3433;
 Best Local Similarity 27.0%; Pred. No. 2.4e+02;
 Matches 10; Conservative 12; Mismatches 5; Indels 10; Gaps 1;
 QY 2 VNTKMFEE-----LKSRDLDTLQAEVALLKEQQ 28
 Db 1895 LNTAIYEDFSQEDSLNKNIKDQLKLGQIAVIEHKQ 1931
 RESULT 13
 DYHC_NEUCR STANDARD; PRT; 4367 AA.
 ID DYHC_NEUCR STANDARD; PRT; 4367 AA.
 AC P45443;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Dynein heavy chain, cytosolic (DYHC).
 GN RO-1.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A;
 RX MEDLINE=95014704; PubMed=7929559;
 RA Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
 RT "Cytoplasmic dynein and actin-related protein Arp1 are required for
 RT normal nuclear distribution in filamentous fungi";
 RL J. Cell Biol. 127:139-149(1994).
 CC -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
 CC MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
 CC ORGANELLES ALONG MICROTUBULES. REQUIRED TO MAINTAIN UNIFORM
 CC NUCLEAR DISTRIBUTION IN HYPHAE.
 CC -!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
 CC INTERMEDIATE AND LIGHT CHAINS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; L31504; AAA64908.1; -;
 DR InterPro; IPR004273; Dynein_heavy.
 DR Pfam; PF03028; Dynein_heavy; 1.
 KW Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
 FT DOMAIN 676 693 COILED COIL (POTENTIAL).
 FT DOMAIN 1176 1215 COILED COIL (POTENTIAL).
 FT DOMAIN 1327 1351 COILED COIL (POTENTIAL).
 FT DOMAIN 1557 1574 COILED COIL (POTENTIAL).
 FT DOMAIN 1637 1668 COILED COIL (POTENTIAL).
 FT DOMAIN 2045 2073 MICROTUBULE-BINDING (POTENTIAL).
 FT DOMAIN 2195 2218 COILED COIL (POTENTIAL).
 FT DOMAIN 3193 3296 COILED COIL (POTENTIAL).
 FT DOMAIN 3423 3481 COILED COIL (POTENTIAL).
 FT DOMAIN 3778 3809 COILED COIL (POTENTIAL).
 FT NP_BIND 1943 1950 ATP (POTENTIAL).
 FT NP_BIND 2240 2247 ATP (POTENTIAL).
 FT NP_BIND 2605 2612 ATP (POTENTIAL).
 FT NP_BIND 2947 2954 ATP (POTENTIAL).
 SQ SEQUENCE 4367 AA; 495568 MW; 1E10F3E2D170D6DF CRC64;
 Query Match 29.9%; Score 51.5; DB 1; Length 4367;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;

Qy 5 KMFELKSRDLTLAGOEVALKE 26
 Db 315 KNEALKERADSLAKEIQYLKD 336

RESULT 15

RA50_THEVO
 ID RA50_THEVO STANDARD; PRT; 895 AA.
 AC P58302;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA double-strand break repair rad50 ATPase.
 GN RAD50 OR TV0228 OR TVG0235331.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Anano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
 CC rad50/mrell complex possesses single-strand endonuclease activity
 CC and ATP-dependent double-strand-specific exonuclease activity.
 CC Rad50 provides an ATP-dependent control of mreII by unwinding
 CC and/or repositioning DNA ends into the mreII active site (By
 CC similarity).
 CC -!- SUBUNIT: Forms a complex with mreII (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AP000991; BAB59370.1; -
 DR InterPro: IPR003439; ABC_transportr.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 KW DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
 FT NP_BIND 30 37 ATP (BY SIMILARITY).
 FT DOMAIN 171 737 COILED COIL (POTENTIAL).
 SQ SEQUENCE 895 AA; 103223 MW; 4A47DA9287E82D3A CRC64;

Query Match 29.7%; Score 51; DB 1; Length 895;
 Best Local Similarity 40.0%; Pred. No. 81;
 Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 3 NTKMFEELKSRDLTLAGOEVALKEQ 27
 Db 202 NKKQTEELKSLRIETPEIKALEEE 226

Search completed: April 15, 2003, 11:48:30
 Job time : 8.5 secs

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:44 ; Search time 11.75 seconds
(without alignments)
294.540 Million cell updates/sec

Title: US-09-445-576a-36

Perfect score: 172

Sequence: 1 VVNTKMFELKSLDLAQEVALLKEQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	202	1	THUN
2	146	84.9	202	2	tetranectin precu
3	84	48.8	166	1	tetranectin homolo
4	60	34.9	761	2	probable thyroid r
5	58	33.7	853	2	hypothetical prote
6	57.5	33.4	279	2	hypothetical 32.1K
7	57	33.1	307	2	D-serine deaminase
8	57	33.1	311	2	D-serine deaminase
9	56	32.6	425	2	seryl-trna synthet
10	55.5	32.3	252	2	hypothetical prote
11	55	32.0	486	2	hypothetical prote
12	54	31.4	126	2	probable hsp prot
13	53.5	31.1	381	2	transcription fact
14	53	30.8	197	2	hypothetical prote
15	53	30.8	222	2	hypothetical prote
16	53	30.8	374	2	hypothetical prote
17	53	30.8	380	2	hypothetical prote
18	53	30.8	616	2	NCA2 protein - yea
19	53	30.8	1034	2	exonuclease SbcC [
20	53	30.8	1043	2	hypothetical prote
21	53	30.8	1549	2	hypothetical prote
22	52.5	30.5	275	2	ribosomal protein
23	52.5	30.5	323	2	homeotic protein v
24	52	30.2	355	2	translation releas
25	52	30.2	524	2	hypothetical prote
26	52	30.2	857	2	ATP-dependent Clp
27	52	30.2	1178	2	probable membrane
28	52	30.2	1356	2	janusin precursor,
29	52	30.2	3433	1	utrophin - human

30	51.5	29.9	4367	1	B54802	dynein heavy chain
31	51	29.7	351	2	A45377	transcription fact
32	51	29.7	498	2	A10458	conserved hypothet
33	51	29.7	597	2	G83990	two-component sens
34	51	29.7	1010	2	B37220	Na+/K+-exchanging
35	51	29.7	1269	2	F84730	probable myosin he
36	51	29.7	1410	1	A57013	early endosome ant
37	50.5	29.4	679	2	S38011	hypothetical prote
38	50	29.1	79	2	AB0012	conserved hypothet
39	50	29.1	181	2	T13518	hypothetical prote
40	50	29.1	224	2	S56809	probable membrane
41	50	29.1	249	1	S75606	serine O-acetyltra
42	50	29.1	349	2	C59107	hypothetical prote
43	50	29.1	369	2	F86714	conserved hypothet
44	50	29.1	394	2	B82931	hypothetical membr
45	50	29.1	502	2	T14286	embryogenic callus

ALIGNMENTS

RESULT 1

THUN

tetranectin precursor [validated] - human
N:Alternate names: plasminogen-kringle 4 binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence:Revision 03-Aug-1995 #text_change 08-Dec-2000
C:Accession: S24126; A56835; A29747; I38359; S19865

R:Berglund, L.; Petersen, T.E.

FEBS Lett. 309, 15-19, 1992

A:Title: The gene structure of tetranectin, a plasminogen binding protein.

A:Reference number: S24126; MUID:92380263; PMID:1511740

A:Accession: S24126

A:Molecule type: DNA

A:Residues: 1-202 <BER>

R:Wewer, U.M.; Albrechtsen, R.

Lab. Invest. 67, 253-262, 1992

A:Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expre

A:Reference number: A56835; MUID:92365345; PMID:1354271

A:Accession: A56835

A:Molecule type: mRNA

A:Residues: 1-202 <WEM>

A:Cross-references: EMBL:X64559; NID:G37408; PIDN:CAA45860.1; PID:G37409

R:Fuhlendorff, J.; Clemmensen, I.; Magnusson, S.

Biochemistry 26, 6757-6764, 1987

A:Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma pro

A:Reference number: A29747; MUID:88107595; PMID:3427041

A:Accession: A29747

A:Molecule type: protein

A:Residues: 22-105, 'G', 107-202 <FUH>

A:Experimental source: plasma

A:Note: 55-Ser and 58-Met were also found

C:Genetics:

A:Gene: GDB:TNA

A:Cross-references: GDB:I35032; OMIM:187520

A:Map position: 3p22-3p21.3

A:Introns: 37/1; 70/1

C:Complex: homotetramer

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: glycoprotein; plasma; tetramer

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-202/Product: tetranectin #status experimental <MAT>

F:71-197/Domain: C-type lectin homology <LCH>

F:25/Binding site: carbohydrate (Thr) (covalent) #status experimental

F:71-81,98-197,173-189/Disulfide bonds: #status experimental

Query Match 100.0%; Score 172; DB 1; Length 202;

Best Local Similarity 100.0%; Pred. No. 1.2e-13;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSLDLTDLAQEVALLKEQALQTVCLK 36

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70575
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: B70575
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-126 <COL>
A: Cross-references: GB:Z95324; GB:AL123456; NID:G3261760; PIDN: CAB08585.1; PID: g2094832
A: Experimental source: strain H37Rv
C: Genetics:
A: Gene: hspR
C: Superfamily: probable heat shock protein merR

Query Match 31.4%; Score 54; DB 2; Length 126;
Best Local Similarity 44.0%; Pred. No. 15;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 TWMFEELKSRDLTLAGVALLKEQ 28
DB 82 TSQVEALQSRLOFMABELAVLRANQ 106

RESULT 13
A54415
Transcription factor HBP-la(c14) - wheat
C: Species: Triticum aestivum (common wheat)
C: Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
C: Accession: A54415
R: Mikami, K.; Sakamoto, A.; Iwabuchi, M.
J. Biol. Chem. 269, 9974-9985, 1994
A: Title: The HBP-1 family of wheat basic/leucine zipper proteins interacts with overlapping
A: Reference number: A54415; MUID: 94193693; PMID: 8144592
A: Accession: A54415
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-381 <MIK>
A: Cross-references: GB:D12920; NID:G5926680; PIDN: BAA02304.1; PID: g497895
C: Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
C: Keywords: DNA binding; transcription factor
F: 297-337/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 31.1%; Score 53.5; DB 2; Length 381;
Best Local Similarity 48.3%; Pred. No. 53;
Matches 14; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 7 FEELKSRDLTLAGVALLKEQ-QALQTV 34
DB 327 WEEVASRADLLKQENSLKEELKQLQK 355

RESULT 14
F64474
hypothetical protein MJ1399 - Methanococcus jannaschii
C: Species: Methanococcus jannaschii
C: Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C: Accession: F64474
R: Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996
A: Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A: Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A: Reference number: A64300; MUID: 96337999; PMID: 8688087
A: Accession: F64474
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA

A: Residues: 1-197 <BUL>
A: Cross-references: GB:U67580; GB:L77117; NID: g1592044; PIDN: AAB99408.1; PID: g1592047
C: Genetics:
A: Map position: REV1359931-1359338
C: Superfamily: hypothetical protein MJ1399

Query Match 30.8%; Score 53; DB 2; Length 197;
Best Local Similarity 47.6%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLTLAGV 21
DB 159 VVNEKSFEDCLNQLDNIQEI 179

RESULT 15
G97129
hypothetical protein CAC1862 [imported] - Clostridium acetobutylicum
C: Species: Clostridium acetobutylicum
C: Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C: Accession: G97129
R: Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A: Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A: Reference number: A96900; MUID: 21359325; PMID: 21359325
A: Accession: G97129
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-222 <KUR>
A: Cross-references: GB:AE001437; PIDN: AAK79826.1; PID: g15024839; GSPDB: GN00168
A: Experimental source: Clostridium acetobutylicum ATCC824
C: Genetics:
A: Gene: CAC1862

Query Match 30.8%; Score 53; DB 2; Length 222;
Best Local Similarity 37.8%; Pred. No. 35;
Matches 17; Conservative 5; Mismatches 11; Indels 12; Gaps 2;

QY 2 VNTKMFELKSRDLTLAGVALLK-----EQALQTVCLK 36
DB 71 VNQKI--EAKKKDTKAEIATFKSEKAKHDEMQRQQTIVLK 113

Search completed: April 15, 2003, 11:51:02
Job time : 13.75 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	172	100.0	36	5	US-09-445-576A-36	Sequence 36, Appl
2	172	100.0	52	5	US-09-445-576A-21	Sequence 71, Appl
3	172	100.0	180	5	US-09-445-576A-77	Sequence 27, Appl
4	172	100.0	181	5	US-09-445-576A-7	Sequence 7, Appl
5	172	100.0	197	5	US-09-445-576A-25	Sequence 25, Appl
6	172	100.0	202	1	PCT-US02-38407-13	Sequence 13, Appl
7	172	100.0	202	5	US-09-992-095B-62	Sequence 62, Appl
8	172	100.0	202	5	US-09-999-570-62	Sequence 62, Appl
9	172	100.0	202	6	US-10-154-678-62	Sequence 62, Appl
10	172	100.0	202	6	US-10-276-781-1559	Sequence 1559, Appl
11	172	100.0	228	5	US-09-445-576A-24	Sequence 24, Appl
12	167	97.1	51	5	US-09-445-576A-35	Sequence 35, Appl
13	162	94.2	52	5	US-09-445-576A-5	Sequence 5, Appl
14	162	94.2	73	5	US-09-445-576A-28	Sequence 28, Appl
15	154	89.5	49	5	US-09-445-576A-6	Sequence 6, Appl
16	154	89.5	65	5	US-09-445-576A-26	Sequence 26, Appl
17	150	87.2	69	5	US-09-445-576A-29	Sequence 29, Appl
18	150	87.2	145	5	US-09-445-576A-31	Sequence 31, Appl
19	150	87.2	330	5	US-09-445-576A-32	Sequence 32, Appl
20	150	87.2	331	5	US-09-445-576A-33	Sequence 33, Appl
21	150	87.2	592	5	US-09-445-576A-34	Sequence 34, Appl
22	146	84.9	36	5	US-09-445-576A-37	Sequence 37, Appl
23	104	60.5	59	5	US-09-513-999C-4342	Sequence 4342, Appl
24	84	48.8	36	5	US-09-445-576A-39	Sequence 39, Appl
25	79	45.9	36	5	US-09-445-576A-38	Sequence 38, Appl
26	75	43.6	197	1	PCT-US02-19669A-55	Sequence 55, Appl

Db 17 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 52

RESULT 3

US-09-445-576A-27
; Sequence 27, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreon Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: H6FTN23
US-09-445-576A-27

Query Match 100.0%; Score 172; DB 5; Length 180;

Best Local Similarity 100.0%; Pred. No. 3.3e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 36

|||||

Db 16 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 51

RESULT 4

US-09-445-576A-7
; Sequence 7, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreon Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mature tetranectin single chain
US-09-445-576A-7

Query Match 100.0%; Score 172; DB 5; Length 181;

Best Local Similarity 100.0%; Pred. No. 3.3e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 36

|||||

Db 17 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 52

RESULT 5

US-09-445-576A-25
; Sequence 25, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreon Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT APPLICATION NUMBER: US/09/445,576A
; CURRENT FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 197
; TYPE: PRT

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: H6FTN123
US-09-445-576A-25

Query Match 100.0%; Score 172; DB 5; Length 197;

Best Local Similarity 100.0%; Pred. No. 3.7e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 36

|||||

Db 33 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 68

RESULT 6

PCT-US02-38407-13
; Sequence 13, Application PC/TUS0238407
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPME
; FILE REFERENCE: D0189
; CURRENT APPLICATION NUMBER: PCT/US02/38407
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,417
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo Sapiens
PCT-US02-38407-13

Query Match 100.0%; Score 172; DB 1; Length 202;

Best Local Similarity 100.0%; Pred. No. 3.8e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 36

|||||

Db 38 VVNTKMFELKSRDLDTLAQEVALLKEQQALQTVCLK 73

RESULT 7

US-09-992-095B-62
; Sequence 62, Application US/09992095B
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US5.DIV
; CURRENT APPLICATION NUMBER: US/09/992,095B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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; LOCATION: 1..21
US-09-992-095B-62

Query Match
Best Local Similarity 100.0%; Score 172; DB 5; Length 202;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 36
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Db 38 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 73

RESULT 8
US-09-999-570-62
; Sequence 62, Application US/09999570
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: G-091US08DIV
; CURRENT FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-09-999-570-62

Query Match
Best Local Similarity 100.0%; Score 172; DB 5; Length 202;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 36
   |||||
Db 38 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 73

RESULT 9
US-10-154-678-62
; Sequence 62, Application US/10154678
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 182.US1.REG
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent
; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-09-999-570-62

Query Match
Best Local Similarity 100.0%; Score 172; DB 5; Length 202;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 36
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Db 38 VVNTKMFEEELKSRDLTLAQEVALLEKEQALQTVCLK 73

RESULT 11
US-09-445-576A-24
; Sequence 24, Application US/09445576A
; GENERAL INFORMATION:
; APPLICANT: Boreau Pharma A/S
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: 62032.000004
; CURRENT FILING DATE: 2000-07-17
; CURRENT APPLICATION NUMBER: US/09/445,576A
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CIIH6FTN123
US-09-445-576A-24

Query Match
Best Local Similarity 100.0%; Score 172; DB 5; Length 228;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LENGTH: 73
TYPE: PRT

Job time : 25.25 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2003, 11:43:14 ; Search time 28.75 seconds
(without alignments)
166.853 Million cell updates/sec

Title: US-09-445-576A-36

Perfect score: 172

Sequence: 1 VVNTKMFEEELKSLTLAQEVALLKEQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	180	AAW94264	H6FXTN23 fusion pr
2	172	100.0	181	AAW94256	Human tetranectin
3	172	100.0	197	AAW94262	H6FXTN123 fusion p
4	172	100.0	202	AAAG0521	Human tetranectin.
5	172	100.0	202	AAAG24034	Human EST encoded
6	172	100.0	228	AAW94261	CLIH6FXTN123 fusio
7	167	97.1	182	AAW60098	Sequence of chain
8	162	94.2	52	AAW94254	Tetranectin polype
9	162	94.2	73	AAW94270	H6FXTripa fusion p
10	154	89.5	49	AAW94255	Tetranectin polype

11	154	89.5	65	20	AAW94263	H6FXTN12 fusion pr
12	150	87.2	69	20	AAW94271	H6FXTripb fusion p
13	150	87.2	145	20	AAW94266	H6FXTripB-UB fusio
14	150	87.2	330	20	AAW94267	H6FXscFv(CEA6)trip
15	150	87.2	331	20	AAW94268	H6FXscFv(CEA6)trip
16	150	87.2	592	20	AAW94269	H6FXscFv(CEA6)trip
17	104	60.5	59	21	AAAG00261	Human secreted pro
18	75	43.6	197	21	AAW82526	Protein encoded by
19	75	43.6	197	23	AAW82642	Human breast tumou
20	75	43.6	206	21	AAW66756	Membrane-bound pro
21	75	43.6	206	22	AAU29161	Human PKO polypept
22	75	43.6	206	22	AAW65279	Human PRO1345 (UNQ
23	75	43.6	206	23	AAE20465	Human tumour-assoc
24	60	34.9	751	22	ABB32409	Peptide #5060 enco
25	60	34.9	751	22	ABB37862	Peptide #5368 enco
26	60	34.9	751	22	ABB23121	Protein #5120 enco
27	60	34.9	751	22	AAW58492	Human brain expres
28	60	34.9	751	22	AAW70992	Human bone marrow
29	60	34.9	751	22	AAW18634	Peptide #5068 enco
30	60	34.9	751	22	AAW31268	Peptide #5305 enco
31	60	34.9	751	22	AAW06199	Peptide #4881 enco
32	60	34.9	751	23	ABG40780	Human peptide enco
33	60	34.9	761	20	AAW28934	CEV14 gene product
34	60	34.9	2017	22	ABG06301	Novel human diagn
35	58	33.7	488	22	ABW64400	Drosophila melanog
36	55	32.0	11	22	AAU24901	Schizophrenia-Asso
37	55	32.0	11	22	AAU15245	Schizophrenia-Asso
38	54	31.4	12	22	AAU24902	Schizophrenia-Asso
39	54	31.4	12	22	AAU15246	Schizophrenia-Asso
40	54	31.4	120	22	AAU70846	C albicans apoptos
41	53.5	31.1	137	23	ABP28176	Streptococcus poly
42	53	30.8	501	21	AAG47543	Arabidopsis thalia
43	53	30.8	505	21	AAG47542	Arabidopsis thalia
44	53	30.8	523	21	AAG47541	Arabidopsis thalia
45	53	30.8	1212	22	ABB71114	Drosophila melanog

ALIGNMENTS

RESULT 1

AAW94264
ID AAW94264 standard; protein; 180 AA.

XX AC AAW94264;

XX DT 26-APR-1999 (first entry)

XX DE H6FXTN23 fusion protein sequence.

XX KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
XX KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
XX KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
XX KW transfection; imaging; tumour; human; tetranectin; H6FXTN23.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09856906-A1.

XX PD 17-DEC-1998.

XX PF 11-JUN-1998; 98WO-DK00245.

XX PR 11-JUN-1997; 97DK-0000685.

XX (ETZE/) ETZERODT M.

PA (GRAV/) GRAVERSEN N J H.

PA (HOLT/) HOLTET T L.

PA (KAST/) KASTRUP J S.

XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;

PI Larsen IK, Nielsen BB, Thøgersen HC;

XX WPI; 1999-080897/07.
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Disclosure; Fig 8; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXTN23 fusion protein sequence. The specification claims
 CC that the heterologous moiety to which the TTSEs of the invention are
 CC linked to is specifically different from the present fusion protein
 CC sequence.
 XX
 XX Sequence 180 AA;

Query Match 100.0%; Score 172; DB 20; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVNTKMFEEKSLRDLTAAQVALLKEQQALQTVCLK 36
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 Db 16 VVNTKMFEEKSLRDLTAAQVALLKEQQALQTVCLK 51

RESULT 2
 AAW94256
 ID AAW94256 standard; protein; 181 AA.
 XX
 AC AAW94256;
 XX
 DT 26-APR-1999 (first entry)
 DE Human tetranectin amino acid sequence.
 DE
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin.
 OS
 XX Homo sapiens.
 XX WO9856906-A1.
 XX 17-DEC-1998.
 XX
 XX 11-JUN-1998; 98WO-DK00245.
 XX

PR 11-JUN-1997; 97DK-0000685.
 XX (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI; 1999-080897/07.
 DR
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 PS Claim 10; Page 60; 110pp; English.

XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a human tetranectin sequence from which the TTSE can be
 CC derived.
 XX
 XX Sequence 181 AA;

Query Match 100.0%; Score 172; DB 20; Length 181;
 Best Local Similarity 100.0%; Pred. No. 7.3e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVNTKMFEEKSLRDLTAAQVALLKEQQALQTVCLK 36
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 Db 17 VVNTKMFEEKSLRDLTAAQVALLKEQQALQTVCLK 52

RESULT 3
 AAW94262
 ID AAW94262 standard; protein; 197 AA.
 XX
 AC AAW94262;
 XX
 DT 26-APR-1999 (first entry)
 DE H6FXTN123 fusion protein sequence.
 DE
 XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; H6FXTN123.
 XX
 OS Homo sapiens.

XX WO9856906-A1.
 XX 17-DEC-1998.
 XX 11-JUN-1998; 98WO-DK00245.
 XX 11-JUN-1997; 97DK-0000685.
 XX (ETZE/) ETZERODT M.
 XX (GRAV/) GRAVERSEN N J H.
 XX (HOLT/) HOLTET T L.
 XX (KAST/) KASTROP J S.
 XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 XX Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI; 1999-080897/07.
 XX New monomer polypeptide constructs for diagnosis and therapy -
 XX comprise a tetranectin trimerising structural element covalently
 XX linked to at least one heterologous moiety for providing functional
 XX activity
 XX Disclosure; Fig 6; 110pp; English.
 XX The invention relates to the design of trimeric polypeptides using
 XX polypeptide structural elements derived from the tetranectin protein
 XX family. The trimeric polypeptides constructed as a monomer polypeptide
 XX construct comprise at least one tetranectin trimerising structural
 XX element (TTSE) which is covalently linked to at least one heterologous
 XX moiety, the TTSE being capable of forming a stable complex with 2 other
 XX TTSEs, with the proviso that the heterologous moiety is different from
 XX any of the fusion proteins CIH6PXTN123, H6FXTN123, H6FXTN23
 XX (AAW94261 to AAW94264). The TTSE can be used for the construction of
 XX conjugates with heterologous moieties such as a ligand binding
 XX structure, a toxin, a detectable label, an in situ activatable substance,
 XX an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 XX a photo cross-linking agent, or a group facilitating conjugation of the
 XX monomer polypeptide construct to a target. They can be used as vehicles
 XX for assembling antibody fragments into oligomeric or multivalent
 XX entities for generating chimeric artificial antibodies having
 XX preselected pharmacokinetic and/or pharmacodynamic properties. The
 XX constructs can be used for targeted gene therapy involving selective
 XX delivery of the material for transfection or infection of the specific
 XX population of cells. They can also be used for delivering a substance to
 XX a cell or tissue or for delivering an imaging or toxin-conjugated
 XX antibody to a tumour. They can also be used for prevention or treating a
 XX disease or for diagnosis. The TTSE provides a stable structure which can
 XX act as a vehicle for a wide variety of conjugates. The present sequence
 XX represents a H6FXTN123 fusion protein sequence. The specification claims
 XX that the heterologous moiety to which the TTSEs of the invention are
 XX linked to is specifically different from the present fusion protein
 XX sequence.

XX SQ Sequence 197 AA;
 Query Match 100.0%; Score 172; DB 20; Length 197;
 Best Local Similarity 100.0%; Pred. No. 8e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 33 VVNTKMFELKSRDLTQAQVALLKEQQAQTVCCLK 68

RESULT 4
 AAR60521
 ID AAR60521 standard; Protein; 202 AA.
 XX AAR60521;
 XX 22-MAR-1995 (first entry)

XX DE Human tetranectin.
 XX KW Serine protease; Factor-Xa; recognition site; tetranectin;
 KW fusion protein cleavage; protein folding; primer;
 KW polymerase chain reaction; amplification.
 XX OS Homo sapiens.
 XX WO9418227-A.
 XX 18-AUG-1994.
 XX 04-FEB-1994; 94WO-DK000054.
 XX 04-FEB-1993; 93DK-0000130.
 XX 05-FEB-1993; 93DK-0000139.
 XX 03-DEC-1993; 93WO-GB02492.
 XX (DENZ-) DENZYME APS.
 XX Etzerodt M, Holtet TL, Thogersen HC;
 XX WPI; 1994-279681/34.
 XX Refolding of polypeptide molecules - using a cyclic process
 XX involving denaturing and renaturing conditions to produce a
 XX correctly folded prod
 XX Disclosure; Page 151-52; 202pp; English.
 XX cDNA encoding human tetranectin (full sequence given in AAR60521) was
 XX PCR amplified using primers given in AA071274-75. Amplified cDNA was
 XX linked to a sequence encoding the Factor-Xa cleavage site (given in
 XX AAR60503), subcloned in vector pT7H6 so that it was linked to a
 XX hexahistidine-encoding sequence and expressed in E. coli BL21. The
 XX fusion protein was purified on an Ni2+-activated NTA-agarose column.
 XX A cyclic procedure was used to obtain correctly folded recombinant
 XX protein.

XX SQ Sequence 202 AA;
 Query Match 100.0%; Score 172; DB 15; Length 202;
 Best Local Similarity 100.0%; Pred. No. 8.3e-14;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRDLTQAQVALLKEQQAQTVCCLK 36
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 Db 38 VVNTKMFELKSRDLTQAQVALLKEQQAQTVCCLK 73

RESULT 5
 AAM24034
 ID AAM24034 standard; Protein; 202 AA.
 XX AAM24034;
 XX 12-OCT-2001 (first entry)
 XX Human EST encoded protein SEQ ID NO: 1559.
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 XX Homo sapiens.
 XX WO200154477-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02687.

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XX  Sequence      228 AA:
Query Match          100.0%; Score 172; DB 20; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.4e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 VVNTKMFELKSRDLTLAGQVALLKEQQAQTVCCLK 36
      |||||||
Db       64 VVNTKMFELKSRDLTLAGQVALLKEQQAQTVCCLK 99

RESULT 7
AAP60098
ID AAP60098 standard; protein; 182 AA.
XX
XX AAP60098;
XX
XX 27-JUN-1991 (first entry)
XX
DE Sequence of chain of Tetranectin protein.
XX
XX Plasminogen activation; clot lysis; fibrinolysis; tissue growth;
XX tissue repair; haemostasis; neoplasia therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 50..60
XX Disulfide-bond 77..176
XX Disulfide-bond 152..168
XX Misc-difference 37
XX /label= M, V
XX
XX EP206400-A.
XX
XX 30-DEC-1986.
XX
PD

```


PA (HOLT/) HOLTET T L.
 XX (KAST/) KASTRUP J S.
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI: 1999-080897/07.
 XX
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 XX Disclosure; Fig 4; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXTripa fusion protein sequence encoded by the plasmid
 CC pH6FXTripa.
 XX
 XX Sequence 73 AA;
 XX
 XX Query Match 94.2%; Score 162; DB 20; Length 73;
 XX Best Local Similarity 97.2%; Pred. No. 4.9e-13;
 XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 VVNTKMFELKSRDLTLAQEVALLKEQQALQTVCLK 36
 Db ||||||||||||||||||||||||||||||||||||
 36 VVNTKMFELKSRDLTLAQEVALLKEQQALQTVSLK 71
 XX
 XX RESULT 10
 XX AAW94255
 XX ID AAW94255 standard; Protein; 49 AA.
 XX AC AAW94255;
 XX
 XX DT 26-APR-1999 (first entry)
 XX
 XX DE Tetranectin polypeptide fragment (residues 1-49).
 XX
 XX KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 XX fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 XX artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 XX transfection; imaging; tumour; human; tetranectin.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO9856906-A1.
 XX
 XX PD 17-DEC-1998.

XX
 PF 11-JUN-1998; 98WO-DK00245.
 XX PR 11-JUN-1997; 97DK-0000685.
 XX
 PA (ETZE/) ETZERODT M.
 PA (GRAV/) GRAVERSEN N J H.
 PA (HOLT/) HOLTET T L.
 PA (KAST/) KASTRUP J S.
 XX
 PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
 PI Larsen IK, Nielsen BB, Thogersen HC;
 XX WPI: 1999-080897/07.
 XX
 XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity
 XX
 XX Example 1; Page 59-60; 110pp; English.
 XX
 CC The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can
 CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a human tetranectin polypeptide fragment. The encoding nucleic
 CC acid sequence was amplified by PCR from the plasmid clone pT7H6FXTN123.
 CC This is used in the construction of E. coli expression vectors for the
 CC production of trimerised chimeric fusion proteins.
 XX
 XX Sequence 49 AA;
 XX
 XX Query Match 89.5%; Score 154; DB 20; Length 49;
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 VVNTKMFELKSRDLTLAQEVALLKEQQALQTV 33
 Db ||||||||||||||||||||||||||||||||
 17 VVNTKMFELKSRDLTLAQEVALLKEQQALQTV 49
 XX
 XX RESULT 11
 XX AAW94263
 XX ID AAW94263 standard; protein; 65 AA.
 XX AC AAW94263;
 XX
 XX DT 26-APR-1999 (first entry)
 XX
 XX DE H6FXTN12 fusion protein sequence.
 XX
 XX KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;

KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
KW transfection; imaging; tumour; human; tetranectin; H6FXTN12.
XX
OS Synhtetic.
OS Homo sapiens.
XX
PN WO9856906-A1.
XX
XX 17-DEC-1998.
XX
XX 11-JUN-1998; 98WO-DK00245.
XX
XX 11-JUN-1997; 97DK-0000685.
XX
PA (ETZE/) ETZERODT M.
PA (GRAV/) GRAVERSEN N J H.
PA (HOLT/) HOLTET T L.
PA (KAST/) KASTRUP J S.
XX
XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
PI Larsen IK, Nielsen BB, Thogersen HC;
XX
XX WPI; 1999-080897/07.
XX
XX New monomer polypeptide constructs for diagnosis and therapy -
PT comprise a tetranectin trimerising structural element covalently
PT linked to at least one heterologous moiety for providing functional
PT activity
XX
XX Disclosure; Fig 8; 110pp; English.
XX
XX The invention relates to the design of trimeric polypeptides using
CC polypeptide structural elements derived from the tetranectin protein
CC family. The trimeric polypeptides constructed as a monomer polypeptide
CC construct comprise at least one tetranectin trimerising structural
CC element (TTSE) which is covalently linked to at least one heterologous
CC moiety, the TTSE being capable of forming a stable complex with 2 other
CC TTSEs, with the proviso that the heterologous moiety is different from
CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
CC conjugates with heterologous moieties such as a ligand binding
CC structure, a toxin, a detectable label, an in situ activatable substance,
CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
CC a photo cross-linking agent, or a group facilitating conjugation of the
CC monomer polypeptide construct to a target. They can be used as vehicles
CC for assembling antibody fragments into oligomeric or multivalent
CC entities for generating chimeric artificial antibodies having
CC preselected pharmacokinetic and/or pharmacodynamic properties. The
CC constructs can be used for targeted gene therapy involving selective
CC delivery of the material for transfection or infection of the specific
CC population of cells. They can also be used for delivering a substance to
CC a cell or tissue or for delivering an imaging or toxin-conjugated
CC antibody to a tumour. They can also be used for prevention or treating a
CC disease or for diagnosis. The TTSE provides a stable structure which can
CC act as a vehicle for a wide variety of conjugates. The present sequence
CC represents a H6FXTN12 fusion protein sequence. The specification claims
CC that the heterologous moiety to which the TTSEs of the invention are
CC linked to is specifically different from the present fusion protein
XX sequence.
XX
SQ Sequence 65 AA;
Query Match 89.5%; Score 154; DB 20; Length 65;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVNTKMFELKSRDLTQAEVALLKEQCALQTV 33
Db 33 VVNTKMFELKSRDLTQAEVALLKEQCALQTV 65
RESULT 12

AAW94271
ID AAW94271 standard; protein; 69 AA.
XX
AC AAW94271;
XX
DT 26-APR-1999 (first entry)
XX
DE H6FXTripb fusion protein sequence.
XX
XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
KW transfection; imaging; tumour; human; tetranectin.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9856906-A1.
XX
XX 17-DEC-1998.
PD
XX
XX 11-JUN-1998; 98WO-DK00245.
XX
XX 11-JUN-1997; 97DK-0000685.
XX
XX (ETZE/) ETZERODT M.
PA (GRAV/) GRAVERSEN N J H.
PA (HOLT/) HOLTET T L.
PA (KAST/) KASTRUP J S.
XX
XX Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;
PI Larsen IK, Nielsen BB, Thogersen HC;
XX
XX WPI; 1999-080897/07.
XX
XX New monomer polypeptide constructs for diagnosis and therapy -
PT comprise a tetranectin trimerising structural element covalently
PT linked to at least one heterologous moiety for providing functional
PT activity
XX
XX Disclosure; Fig 4; 110pp; English.
XX
XX The invention relates to the design of trimeric polypeptides using
CC polypeptide structural elements derived from the tetranectin protein
CC family. The trimeric polypeptides constructed as a monomer polypeptide
CC construct comprise at least one tetranectin trimerising structural
CC element (TTSE) which is covalently linked to at least one heterologous
CC moiety, the TTSE being capable of forming a stable complex with 2 other
CC TTSEs, with the proviso that the heterologous moiety is different from
CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
CC conjugates with heterologous moieties such as a ligand binding
CC structure, a toxin, a detectable label, an in situ activatable substance,
CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
CC a photo cross-linking agent, or a group facilitating conjugation of the
CC monomer polypeptide construct to a target. They can be used as vehicles
CC for assembling antibody fragments into oligomeric or multivalent
CC entities for generating chimeric artificial antibodies having
CC preselected pharmacokinetic and/or pharmacodynamic properties. The
CC constructs can be used for targeted gene therapy involving selective
CC delivery of the material for transfection or infection of the specific
CC population of cells. They can also be used for delivering a substance to
CC a cell or tissue or for delivering an imaging or toxin-conjugated
CC antibody to a tumour. They can also be used for prevention or treating a
CC disease or for diagnosis. The TTSE provides a stable structure which can
CC act as a vehicle for a wide variety of conjugates. The present sequence
CC represents a H6FXTripb fusion protein sequence. The present sequence
CC represents a H6FXTripb fusion protein sequence encoded by the plasmid
CC pH6FXTripb.
XX
SQ Sequence 69 AA;
Query Match 87.2%; Score 150; DB 20; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLTQAQVALLKEQALQT 32
 |||||
 Db 36 VVNTKMFELKSRDLTQAQVALLKEQALQT 67

RESULT 13

AAW94266
 ID AAW94266 standard; protein; 145 AA.

AC AAW94266;

DT 26-APR-1999 (first entry)

DE H6FXtripB-UB fusion protein sequence.

XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; ubiquitin.

XX Synthetic.

OS Homo sapiens.

PN WO9856906-A1.

XX 17-DEC-1998.

PF 11-JUN-1998; 98WO-DK00245.

PR 11-JUN-1997; 97DK-0000685.

PA (ETZE/) ETZERODT M.

PA (GRAV/) GRAVERSEN N J H.

PA (HOLT/) HOLTET T L.

PA (KAST/) KASTRUP J S.

PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;

PI Larsen IK, Nielsen BB, Thogersen HC;

DR WPI; 1999-080897/07.

XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity

PS Example 3; Fig 14; 110pp; English.

XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent
 CC entities for generating chimeric artificial antibodies having
 CC preselected pharmacokinetic and/or pharmacodynamic properties. The
 CC constructs can be used for targeted gene therapy involving selective
 CC delivery of the material for transfection or infection of the specific
 CC population of cells. They can also be used for delivering a substance to
 CC a cell or tissue or for delivering an imaging or toxin-conjugated
 CC antibody to a tumour. They can also be used for prevention or treating a
 CC disease or for diagnosis. The TTSE provides a stable structure which can

CC act as a vehicle for a wide variety of conjugates. The present sequence
 CC represents a H6FXtripB-UB (ubiquitin) fusion protein sequence encoded by
 CC the plasmid pH6FXtripB-UB.

XX Sequence 145 AA;

Query Match 87.2%; Score 150; DB 20; Length 145;
 Best Local Similarity 100.0%; Pred. No. 3.3e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVNTKMFELKSRDLTQAQVALLKEQALQT 32
 |||||
 Db 36 VVNTKMFELKSRDLTQAQVALLKEQALQT 67

RESULT 14

AAW94267

ID AAW94267 standard; protein; 330 AA.

XX AAW94267;

DT 26-APR-1999 (first entry)

DE H6FXscFv(CEA6)tripB fusion protein sequence.

XX Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
 KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
 KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
 KW transfection; imaging; tumour; human; tetranectin; CEA6.

XX Synthetic.

OS Homo sapiens.

PN WO9856906-A1.

XX 17-DEC-1998.

PF 11-JUN-1998; 98WO-DK00245.

PR 11-JUN-1997; 97DK-0000685.

PA (ETZE/) ETZERODT M.

PA (GRAV/) GRAVERSEN N J H.

PA (HOLT/) HOLTET T L.

PA (KAST/) KASTRUP J S.

PI Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS;

PI Larsen IK, Nielsen BB, Thogersen HC;

DR WPI; 1999-080897/07.

XX New monomer polypeptide constructs for diagnosis and therapy -
 PT comprise a tetranectin trimerising structural element covalently
 PT linked to at least one heterologous moiety for providing functional
 PT activity

PS Example 4; Fig 16; 110pp; English.

XX The invention relates to the design of trimeric polypeptides using
 CC polypeptide structural elements derived from the tetranectin protein
 CC family. The trimeric polypeptides constructed as a monomer polypeptide
 CC construct comprise at least one tetranectin trimerising structural
 CC element (TTSE) which is covalently linked to at least one heterologous
 CC moiety, the TTSE being capable of forming a stable complex with 2 other
 CC TTSEs, with the proviso that the heterologous moiety is different from
 CC any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
 CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
 CC conjugates with heterologous moieties such as a ligand binding
 CC structure, a toxin, a detectable label, an in situ activatable substance,
 CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
 CC a photo cross-linking agent, or a group facilitating conjugation of the
 CC monomer polypeptide construct to a target. They can be used as vehicles
 CC for assembling antibody fragments into oligomeric or multivalent

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:45:59 ; Search time 10 Seconds
(without alignments)
105.923 Million cell updates/sec

Title: US-09-445-576A-36

Perfect score: 172

Sequence: 1 VVNTKMFEEKSLRLDTLAQEVALLKEQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	202	1	US-08-469-486-56
2	172	100.0	202	2	US-08-469-658-56
3	75	43.6	197	4	US-09-602-877A-99
4	52	30.2	1358	1	US-08-404-665-4
5	52	30.2	1358	1	US-08-404-671-4
6	52	30.2	1358	1	US-08-404-781-4
7	50	29.1	169	4	US-09-183-861-41
8	50	29.1	169	4	US-09-022-765-41
9	50	29.1	504	2	US-08-645-900A-1
10	50	29.1	504	2	US-08-882-238A-1
11	50	29.1	504	2	US-08-667-790A-1
12	50	29.1	504	4	US-09-220-459-1
13	50	29.1	504	4	US-08-938-669A-32
14	50	29.1	504	4	US-08-546-568B-1
15	50	29.1	504	4	US-09-056-285A-8
16	50	29.1	835	2	US-08-968-751-4
17	49	28.5	287	1	US-07-952-817-24
18	49	28.5	1627	1	US-07-665-792B-9
19	48.5	28.2	718	3	US-09-090-808-2
20	48.5	28.2	718	4	US-09-447-453-2
21	48	27.9	133	4	US-09-134-001C-5352
22	48	27.9	528	4	US-08-928-213B-8
23	48	27.9	657	4	US-09-370-368-7
24	48	27.9	1235	2	US-08-680-326-36
25	47.5	27.6	514	4	US-08-796-899-25
26	47.5	27.6	561	3	US-09-192-545-2
27	47	27.3	413	3	US-08-669-408B-10

28	47	27.3	1024	4	US-09-562-737-86	Sequence 86, Appl
29	46	26.7	48	2	US-08-743-200-8	Sequence 8, Appl
30	46	26.7	65	2	US-08-867-087B-37	Sequence 37, Appl
31	46	26.7	99	2	US-08-710-749-10	Sequence 10, Appl
32	46	26.7	99	2	US-08-710-749-11	Sequence 11, Appl
33	46	26.7	99	2	US-08-710-749-12	Sequence 12, Appl
34	46	26.7	288	3	US-08-312-949-4	Sequence 4, Appl
35	46	26.7	288	3	US-08-446-201-4	Sequence 4, Appl
36	46	26.7	289	1	US-08-072-070-4	Sequence 4, Appl
37	46	26.7	289	1	US-08-469-434-4	Sequence 4, Appl
38	46	26.7	289	1	US-08-214-222-4	Sequence 4, Appl
39	46	26.7	289	2	US-08-467-852A-5	Sequence 5, Appl
40	46	26.7	289	2	US-08-468-718-4	Sequence 4, Appl
41	46	26.7	289	2	US-08-247-491A-5	Sequence 5, Appl
42	46	26.7	310	1	US-08-129-456A-36	Sequence 36, Appl
43	46	26.7	310	2	US-08-705-868-3	Sequence 3, Appl
44	46	26.7	310	3	US-09-123-615-3	Sequence 3, Appl
45	46	26.7	310	4	US-08-360-821B-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-469-486-56
; Sequence 56, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoeegensen, Hans Christian
; APPLICANT: Holtet, Thor Las
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-56

Query Match 100.0%; Score 172; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;

Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVNTKMFEEKSRDLTLAQEVALLKEQQAQTVCCLK 36
 |||||
 Db 38 VVNTKMFEEKSRDLTLAQEVALLKEQQAQTVCCLK 73

RESULT 2

US-08-469-658-56
 ; Sequence 56, Application US/08469658
 ; Patent No. 5917018

GENERAL INFORMATION:

; APPLICANT: Th egersen, Hans Christian

; APPLICANT: Holtet, Thor Las

; APPLICANT: Etzerodt, Michael

; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/469,658

; FILING DATE: June 5, 1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/192,060

; FILING DATE: February 4, 1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul T. Clark

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 06363/002002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617 542 5070

; TELEFAX: 617 542 8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 56:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 202 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-469-658-56

Query Match 100.0%; Score 172; DB 2; Length 202;

Best Local Similarity 100.0%; Pred. No. 3.5e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVNTKMFEEKSRDLTLAQEVALLKEQQAQTVCCLK 36
 |||||
 Db 38 VVNTKMFEEKSRDLTLAQEVALLKEQQAQTVCCLK 73

RESULT 3

US-09-602-877A-99

; Sequence 99, Application US/09602877A

; Patent No. 6432707

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.446C5

; CURRENT APPLICATION NUMBER: US/09/602,877A

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 99

; LENGTH: 197

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-602-877A-99

Query Match

43.6%; Score 75; DB 4; Length 197;

Best Local Similarity 57.1%; Pred. No. 0.0059;

Matches 16; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 9 ELKSRDLTLAQEVALLKEQQAQTVCCLK 36
 :|||::: || ||| |||||:::

Db 43 DLKQTIEKLWTEVNALKEIQALQTVCLR 70

RESULT 4

US-08-404-665-4

; Sequence 4, Application US/08404665

; Patent No. 5591583

; GENERAL INFORMATION:

; APPLICANT: Reid, Robert A.

; APPLICANT: Ackley, Rhonda L.

; APPLICANT: Hemperly, John J.

; TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and

; ADDRESSEE: Company

; STREET: 1 Becton Drive

; CITY: Franklin Lakes

; STATE: NJ

; COUNTRY: US

; ZIP: 07417

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/404,665

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Fugit, Donna R.

; REGISTRATION NUMBER: 32,135

; REFERENCE/DOCKET NUMBER: P-3341

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1358 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-404-665-4

Query Match 30.2%; Score 52; DB 1; Length 1358;

Best Local Similarity 36.0%; Pred. No. 80;

Matches 9; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 3 NTKMFEEKSRDLTLAQEVALLKEQ 27
 : : : : ||| : : : : | : : : : |

Db 130 SAQVQLQELLSRIEMLEREVSRLRQ 154

RESULT 5

US-09-183-861-41

Query Match 29.1%; Score 50; DB 4; Length 169;
 Best Local Similarity 54.5%; Pred. No. 13;
 Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 8 BELKSRLDTLAEVALLKEQQA 29
 |||: |||| | : | : | : |
 Db 144 EELQRLDTATQRAELEAQA 165

RESULT 8

US-09-022-765-41
 ; Sequence 41, Application US/09022765
 ; Patent No. 6375955
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/022.765
 ; FILING DATE: 12-FEB-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.420C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 169 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Leishmania major

US-09-022-765-41

Query Match 29.1%; Score 50; DB 4; Length 169;
 Best Local Similarity 54.5%; Pred. No. 13;
 Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 8 BELKSRLDTLAEVALLKEQQA 29
 |||: |||| | : | : | : |
 Db 144 EELQRLDTATQRAELEAQA 165

RESULT 9

US-08-645-900A-1
 ; Sequence 1, Application US/08645900A
 ; Patent No. 5849879
 ; GENERAL INFORMATION:
 ; APPLICANT: NGUYEN, THAI D.
 ; APPLICANT: POLANSKY, JON R.

; APPLICANT: HUANG, WEIDONG
 ; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
 ; TITLE OF INVENTION: GLAUCOMA
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOWREY & SIMON
 ; STREET: 1299 PENNSYLVANIA AVE., N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: US
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/645.900A
 ; FILING DATE: 14 MAY 1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MARSH, DAVID
 ; REGISTRATION NUMBER: 41,408
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 383-7451
 ; TELEFAX: (202) 383-6610
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 504 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 5849879e
 ; US-08-645-900A-1

Query Match 29.1%; Score 50; DB 2; Length 504;
 Best Local Similarity 48.0%; Pred. No. 46;
 Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 8 BELKSRLDTLAEVALLKEQQAQQT 32
 | | | | | : | | | | : | | |
 Db 164 ENLARRLESSQVEVARLRGQCQFOT 188

RESULT 10

US-08-882-238A-1
 ; Sequence 1, Application US/08882238A
 ; Patent No. 5854415
 ; GENERAL INFORMATION:
 ; APPLICANT: NGUYEN, THAI D.
 ; APPLICANT: POLANSKY, JON R.
 ; APPLICANT: HUANG, WEIDONG
 ; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
 ; TITLE OF INVENTION: GLAUCOMA
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOWREY & SIMON
 ; STREET: 1299 PENNSYLVANIA AVE., N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: US
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882.238A
 ; FILING DATE: 25 JUNE 1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MARSH, DAVID

REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5854415e
US-08-882-238A-1

Query Match 29.1%; Score 50; DB 2; Length 504;
Best Local Similarity 48.0%; Pred. No. 46;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQQAQLOT 32
| | | | | : | | | | | : | | |
Db 164 ENLARRLESSQVEVARLRGQCPT 188

RESULT 11

US-08-667-790A-1
Sequence 1, Application US/08667790A
Patent No. 5861497
GENERAL INFORMATION:

APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: HUANG, WEIDONG
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
TITLE OF INVENTION: GLAUCOMA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,790A
FILING DATE: 21 JUNE 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARSH, DAVID
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5861497e
US-08-667-790A-1

Query Match 29.1%; Score 50; DB 2; Length 504;
Best Local Similarity 48.0%; Pred. No. 46;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQQAQLOT 32
| | | | | : | | | | | : | | |
Db 164 ENLARRLESSQVEVARLRGQCPT 188

RESULT 12
US-09-220-459-1
Sequence 1, Application US/09220459
Patent No. 6150161
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D
APPLICANT: Polansky, Jon R
APPLICANT: Huang, Weidong
TITLE OF INVENTION: Methods for the Diagnosis of Glaucoma
FILE REFERENCE: 07425.0056
CURRENT APPLICATION NUMBER: US/09/220,459
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 08/882,238
EARLIER FILING DATE: 1997-06-25
EARLIER APPLICATION NUMBER: 08/649,432
EARLIER FILING DATE: 1996-05-17
EARLIER APPLICATION NUMBER: 08/546,568
EARLIER FILING DATE: 1995-10-20
EARLIER APPLICATION NUMBER: 08/336,235
EARLIER FILING DATE: 1994-11-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
US-09-220-459-1

Query Match 29.1%; Score 50; DB 4; Length 504;
Best Local Similarity 48.0%; Pred. No. 46;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQQAQLOT 32
| | | | | : | | | | | : | | |
Db 164 ENLARRLESSQVEVARLRGQCPT 188

RESULT 13

US-08-938-669A-32
Sequence 32, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857

TELEFAX: 202 383-6610
TELEX:

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

US-08-938-669A-32

Query Match 29.1%; Score 50; DB 4; Length 504;

Best Local Similarity 48.0%; Pred. No. 46;

Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQALQT 32

Db 164 ENLARRLESSQVEARLRRCGPOT 188

RESULT 14

US-08-546-568B-1

Sequence 1, Application us/08546568B

Patent No. 6248867

GENERAL INFORMATION:

APPLICANT: NGUYEN, THAI D.

APPLICANT: POLANSKY, JON R.

APPLICANT: HUANG, WEIDONG

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF

TITLE OF INVENTION: GLAUCOMA

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWREY & SIMON

STREET: 1299 PENNSYLVANIA AVE., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: US

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/546,568B

FILING DATE: 20 October 1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: MARSH, DAVID

REGISTRATION NUMBER: 41,408

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 383-7451

TELEFAX: (202) 383-6610

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6248867e

US-08-546-568B-1

Query Match

Best Local Similarity 29.1%; Score 50; DB 4; Length 504;

Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQALQT 32

Db 164 ENLARRLESSQVEARLRRCGPOT 188

RESULT 15

US-09-056-285A-8

Sequence 8, Application US/09056285A

Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.

APPLICANT: Sheffield, Val C.

APPLICANT: Alward, Wallace L.M.

APPLICANT: Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,285A

FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: UIA-010.28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-056-285A-8

Query Match

Best Local Similarity 29.1%; Score 50; DB 4; Length 504;

Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 8 BELKSRDLTQAQVALLKEQALQT 32

Db 164 ENLARRLESSQVEARLRRCGPOT 188

Search completed: April 15, 2003, 11:51:48

Job time : 12 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	172	100.0	362	9	US-09-987-107-39	Sequence 39, Appl
2	172	100.0	202	9	US-09-924-340-62	Sequence 62, Appl
3	172	100.0	202	9	US-09-992-600A-62	Sequence 62, Appl
4	167	97.1	51	9	US-09-987-107-12	Sequence 12, Appl
5	162	94.2	58	9	US-09-987-107-13	Sequence 13, Appl
6	162	94.2	258	9	US-09-987-107-4	Sequence 4, Appl
7	162	94.2	273	9	US-09-987-107-50	Sequence 50, Appl
8	162	94.2	301	9	US-09-987-107-3	Sequence 3, Appl
9	162	94.2	301	9	US-09-987-107-5	Sequence 5, Appl
10	162	94.2	304	9	US-09-987-107-6	Sequence 6, Appl
11	162	94.2	304	9	US-09-987-107-7	Sequence 7, Appl
12	162	94.2	304	9	US-09-987-107-8	Sequence 8, Appl
13	162	94.2	306	9	US-09-987-107-9	Sequence 9, Appl
14	162	94.2	306	9	US-09-987-107-10	Sequence 10, Appl
15	162	94.2	306	9	US-09-987-107-11	Sequence 11, Appl
16	162	94.2	316	9	US-09-987-107-48	Sequence 48, Appl
17	162	94.2	316	9	US-09-987-107-54	Sequence 54, Appl
18	162	94.2	323	9	US-09-987-107-56	Sequence 56, Appl
19	162	94.2	323	9	US-09-987-107-58	Sequence 58, Appl

RESULT 2
US-09-924-340-62
; Sequence 62, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION: Stéphane
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND

QY 1 VVNTKMFEEKLSRLDTLAEVALLKEQALQTVCLK 36
| | | | | | | | | | | | | | | | | | | | | |
Db 38 VVNTKMFEEKLSRLDTLAEVALLKEQALQTVCLK 73

Query Match	94.2%	Score 162;	DB 9;	Length 58;
Best Local Similarity	97.2%	Pred. No. 1.2e-14;		
Matches 35; Conservative	0;	Mismatches 1;	Indels	


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RESULT 9
US-09-987-107-5
; Sequence 5, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987.107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 301
; TYPE: PPT

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RESULT 10

; SEQ ID NO 6

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/ AFFILIATI: ROESTRUP, SOLEN
/
/ TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
/
/ FILE REFERENCE: GRAVERSENIA
/
/ CURRENT APPLICATION NUMBER: US/09/987,107
/
/ CURRENT FILING DATE: 2001-11-13
/
/ PRIOR APPLICATION NUMBER: US 60/264,022
/
/ PRIOR FILING DATE: 2001-01-26
/
/ PRIOR APPLICATION NUMBER: DK PA2001 00057
/
/ PRIOR FILING DATE: 2001-01-15
/
/ PRIOR APPLICATION NUMBER: DK PA2000 01682
/
/ PRIOR FILING DATE: 2000-11-10
/
/ NUMBER OF SEQ ID NOS: 91
/
/ SOFTWARE: PatentIn version 3.1
/

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; SEQ ID NO 8
; LENGTH: 304
; TYPE: PRT
; ORGANISM: H

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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(56)
: OTHER INFORMATION: Trimerisation module from tetranectin
: NAME/KEY: misc_feature
: LOCATION: (13)..(13)
: OTHER INFORMATION: Mutagen
: NAME/KEY: misc_feature
: LOCATION: (19)..(19)
: OTHER INFORMATION: Mutagen
:

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US-09-987-107-7
; Sequence 7, Application US/09987107
; Patent No. US20020156007A1

; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo A1
US-09-987-107-8

Query Match 94.2%; Score 162; DB 9; Length 304;
Best Local Similarity 97.2%; Pred. No. 8.7e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 36
|||||
Db 21 VVNTKMFELKSRDLTLAQEVALLKEQALQTVSLK 56

RESULT 13

US-09-987-107-9
; Sequence 9, Application US/09987107
; Patent No. US20020156007A1

; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(58)

; OTHER INFORMATION: Trimerisation module from tetranectin

; NAME/KEY: misc_feature

; LOCATION: (59)..(63)

; OTHER INFORMATION: Linker

; NAME/KEY: misc_feature

; LOCATION: (64)..(306)

; OTHER INFORMATION: Mature Apo A1

US-09-987-107-9

Query Match 94.2%; Score 162; DB 9; Length 306;

Best Local Similarity 97.2%; Pred. No. 8.8e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 36
|||||
Db 21 VVNTKMFELKSRDLTLAQEVALLKEQALQTVSLK 56

RESULT 14

US-09-987-107-10
; Sequence 10, Application US/09987107
; Patent No. US20020156007A1

; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15

; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(56)

; OTHER INFORMATION: Trimerisation module from tetranectin

; NAME/KEY: misc_feature

; LOCATION: (57)..(63)

; OTHER INFORMATION: Tetranectin based linker

; NAME/KEY: misc_feature

; LOCATION: (64)..(306)

; OTHER INFORMATION: Mature Apo A1

US-09-987-107-10

Query Match 94.2%; Score 162; DB 9; Length 306;

Best Local Similarity 97.2%; Pred. No. 8.8e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRDLTLAQEVALLKEQALQTVCLK 36
|||||
Db 21 VVNTKMFELKSRDLTLAQEVALLKEQALQTVSLK 56

RESULT 15

US-09-987-107-11

; Sequence 11, Application US/09987107

; Patent No. US20020156007A1

; GENERAL INFORMATION:

; APPLICANT: GRAVERSEN, Jonas

; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES

; FILE REFERENCE: GRAVERSENIA

; CURRENT APPLICATION NUMBER: US/09/987,107

; CURRENT FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/264,022

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: DK PA2001 00057

; PRIOR FILING DATE: 2001-01-15

; PRIOR APPLICATION NUMBER: DK PA2000 01682

; PRIOR FILING DATE: 2000-11-10

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(56)

; OTHER INFORMATION: Trimerisation module from tetranectin

; NAME/KEY: misc_feature

; LOCATION: (13)..(13)

; OTHER INFORMATION: Mutagen

; NAME/KEY: misc_feature

; LOCATION: (19)..(19)

; OTHER INFORMATION: Mutagen

; NAME/KEY: misc_feature

; LOCATION: (57)..(63)

; OTHER INFORMATION: tetranectin based linker

; NAME/KEY: misc_feature

; LOCATION: (64)..(306)

; OTHER INFORMATION: Mature Apo A1

US-09-987-107-11

Query Match 94.2%; Score 162; DB 9; Length 306;

Best Local Similarity 97.2%; Pred. No. 8.8e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: April 15, 2003, 12:06:34
Job time : 11 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2003, 11:48:05 ; Search time 183 Seconds
(without alignments)
126.833 Million cell updates/sec

Title: US-09-445-576A-36

Perfect score: 172

Sequence: 1 VVNTMFEEKSLRLDTLAQEVALLKEQALQTVCLK 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	36	18 US-09-445-576-35	Sequence 35, Appl
2	172	100.0	36	23 US-09-987-107-39	Sequence 39, Appl
3	172	100.0	95	22 US-09-834-366-13425	Sequence 13425, A
4	172	100.0	95	27 US-60-197-873-13425	Sequence 13425, A
5	172	100.0	180	18 US-09-445-576-27	Sequence 27, Appl
6	172	100.0	181	18 US-09-445-576-7	Sequence 7, Appl

7	172	100.0	197	18	US-09-445-576-25	Sequence 25, Appl
8	172	100.0	202	21	US-09-791-537-41342	Sequence 41342, A
9	172	100.0	202	23	US-09-924-340-62	Sequence 62, Appl
10	172	100.0	202	23	US-09-992-600A-62	Sequence 62, Appl
11	172	100.0	202	23	US-09-994-590-62	Sequence 62, Appl
12	172	100.0	202	24	US-10-000-489-62	Sequence 62, Appl
13	172	100.0	202	24	US-10-000-986-62	Sequence 62, Appl
14	172	100.0	202	27	US-60-305-456-62	Sequence 62, Appl
15	172	100.0	202	27	US-60-365-384-579	Sequence 579, Appl
16	172	100.0	228	18	US-09-445-576-24	Sequence 24, Appl
17	172	100.0	254	26	US-10-238-659-667	Sequence 667, Appl
18	172	100.0	268	26	US-10-238-659-450	Sequence 450, Appl
19	169	98.3	182	21	US-09-791-537-88542	Sequence 88542, A
20	167	97.1	51	23	US-09-987-107-12	Sequence 12, Appl
21	162	94.2	52	18	US-09-445-576-5	Sequence 5, Appl
22	162	94.2	58	23	US-09-987-107-13	Sequence 13, Appl
23	162	94.2	73	18	US-09-445-576-28	Sequence 28, Appl
24	162	94.2	258	23	US-09-987-107-4	Sequence 4, Appl
25	162	94.2	273	23	US-09-987-107-50	Sequence 50, Appl
26	162	94.2	301	23	US-09-987-107-3	Sequence 3, Appl
27	162	94.2	301	23	US-09-987-107-5	Sequence 5, Appl
28	162	94.2	304	23	US-09-987-107-6	Sequence 6, Appl
29	162	94.2	304	23	US-09-987-107-7	Sequence 7, Appl
30	162	94.2	304	23	US-09-987-107-8	Sequence 8, Appl
31	162	94.2	306	23	US-09-987-107-9	Sequence 9, Appl
32	162	94.2	306	23	US-09-987-107-10	Sequence 10, Appl
33	162	94.2	306	23	US-09-987-107-11	Sequence 11, Appl
34	162	94.2	316	23	US-09-987-107-48	Sequence 48, Appl
35	162	94.2	316	23	US-09-987-107-54	Sequence 54, Appl
36	162	94.2	323	23	US-09-987-107-56	Sequence 56, Appl
37	162	94.2	323	23	US-09-987-107-58	Sequence 58, Appl
38	162	94.2	323	23	US-09-987-107-60	Sequence 60, Appl
39	162	94.2	324	23	US-09-987-107-62	Sequence 62, Appl
40	162	94.2	324	23	US-09-987-107-64	Sequence 64, Appl
41	162	94.2	324	23	US-09-987-107-66	Sequence 66, Appl
42	154	89.5	49	18	US-09-445-576-6	Sequence 6, Appl
43	154	89.5	65	18	US-09-445-576-26	Sequence 26, Appl
44	150	87.2	69	18	US-09-445-576-29	Sequence 29, Appl
45	150	87.2	145	18	US-09-445-576-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-445-576-35
; Sequence 35, Application US/09445576
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Hans Christian
; APPLICANT: Etzerodt, Michael
; APPLICANT: Holtet, Thor Las
; APPLICANT: Graversen, Niels Jonas Heilskov
; APPLICANT: Kastrup, Jette Sandholm
; APPLICANT: Nielsen, Bettina Bryde
; APPLICANT: Larsen, Ingrid Kjoeller
; TITLE OF INVENTION: Trimerising module
; FILE REFERENCE: THOGERSEN =1
; CURRENT APPLICATION NUMBER: US/09/445,576
; CURRENT FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: PCT/DK98/00245
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: DK 0685/97
; PRIOR FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 36
; TYPE: PRT
; ORGANISM: human
US-09-445-576-35

Query Match 100.0%; Score 172; DB 18; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-15;


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; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-10-000-986-62

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Best Local Similarity 100.0%; Pred. No. 9.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVNTKMFELKSRLDTLAEVALLKEQQALQTVCLK 36
    |||||||||||||||||||||||||||||||||||
Db 38 VVNTKMFELKSRLDTLAEVALLKEQQALQTVCLK 73

RESULT 14
US-60-305-456-62
; Sequence 62, Application US/60305456
; GENERAL INFORMATION:
; APPLICANT: BEJANIN, Stephane
; APPLICANT: TANAKA, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
; FILE REFERENCE: 97.USS.PRO
; CURRENT APPLICATION NUMBER: US/60/305.456
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-305-456-62

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Best Local Similarity 100.0%; Pred. No. 9.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 38 VVNTKMFELKSRLDTLAEVALLKEQQALQTVCLK 73

RESULT 15
US-60-365-384-579
; Sequence 579, Application US/60365384
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Zhao, Qing A.
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Weng, Gezhi
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 814
; CURRENT APPLICATION NUMBER: US/60/365.384
; CURRENT FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 579
; LENGTH: 202
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-60-365-384-579

Query Match          100.0%; Score 172; DB 27; Length 202;
Best Local Similarity 100.0%; Pred. No. 9.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 38 VVNTKMFELKSRLDTLAEVALLKEQQALQTVCLK 73

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